GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.	process a process against the process of the proces	on: February 17, 2006, 03:42:53 ; Search time 168.444 Seconds (Without alignments) 93.904 Million cell updates/sec	Title: US-09-830-972A-2_COPY_1090_1125		Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5	rrched: 2443163 seqs, 439378781 residues	Total number of hits satisfying chosen parameters: 2443163	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries	abase : A_Geneseq_21:* 1: geneseqp1908:* 2: geneseqp20008:* 3: geneseqp20018:* 4: geneseqp2018:* 5: geneseqp2018:* 6: geneseqp20038:* 7: geneseqp20038:* 9: geneseqp20038:*
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The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively central nervous system (CNS) myelin material with which it is natively central nervous system (CNS) myelin material with which it is natively central nervous special contents. The content of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, cependyoma, pinealoma, heamangioblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Content production of Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis can be used to inhibit production of Nogo protein to induce regeneration of neuring growth, regeneration or maintenance are deficient or desired. The neuring growth, regeneration or maintenance are deficient or desired. The animal models can be used in disagnestic and screening methods for animal models can be used in disagnestic and screening methods for content or disorders and to screen for or test molecules which can be read in disagnestic of maintenance and composed of His-tag/TV-tag/Nogo-C referent for or test molecules which can be read in this or or test molecules which can be read in diseases of the CNS. The present sequence is derived by fusing two fragments from rat Nogo C and Nogo A sequence or prevent disorders or diseases of the CNS. The present eadletion, where in the construction of mutant Nogo-C which is since of Nogo protein. Major inhibitory region was identified in the Nogo sequence from amino acids 172-974, particularly amino acids 542-722. In a sequence from mino acids 172-974, particularly amino acids 542-722. In Captoblast spreading. Note: The present sequence is not given in the Sequence shown in Apy11310. SEQ ID numbers 35-42 are referred much Nogo-A sequence shown in Apy11310. SEQ ID numbers for these SEQ ID contents and Nogo A sequence shown in Apy11310. SEQ ID numbers for the specification does not include sequence f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 100.0%; Score 175; DB 3; Local Similarity 100.0%; Pred. No. 3.8e-16; Lec 36; Conservative 0; Mismatches 0;
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98IL-00124500. 98WO-US014715. 98US-00218277. 99US-00314161.

21-JUL-1998; 22-DEC-1998; 19-MAY-1999;

19-MAY-1998;

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The invention relates to promoting nerve regeneration or conferring cartral/peripheral nervous system (NS). The method involves administering cartral/peripheral nervous system (NS). The method involves administering CC central/peripheral nervous system (NS). The method involves administering peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system of form injury/disease, where the injury is spiral cord injury, blunt for trauma, penetrating trauma, hemorrhapic stroke, ischaemic stroke or damages caused by surgery such as tumour excision. The disease is not an excimance in eneropathy so in enoplasm. The disease is not an adequencation of process occurring in either gray or white matter or both. The disease is concerned in eneropathy, senile dementia, Alzahamer's disease, parkinson's disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and concerned is a crentification, prion diseases such virtual neficiency, intervertebral dise herniation, prion diseases such concerned and prophyria, hypoglycemia, Sjorgren Larseon syndrome, acute concerned by pophyria, hypoglycemia, Sjorgren Larseon syndrome, acute concerned by oblycythemia vera, immunoglobulin (Ig)A- and IgG gamma-constructive lung diseases, acromegaly, malabsorption or syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-completions, observations of various drugs (e.g., metropathy, allabsorption constructive lung diseases, acromegaly, malabsorption constructive lung diseases, acromegaly, malabsorption actarians of various drugs (e.g., metropathy, allabsorption constructive lung diseases, acromegaly, malabsorption actarians of various drugs (e.g., metropathy, allabsorption and the present sequence represents the rate of an example of NS-specific constructive lung persons acromed and proprofetional and proprofetion p
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                                                                                                                                                                                    Promoting nerve regeneration and preventing neuronal degeneration in the central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated I cells/antigen, or analogs/peptides.
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                                       Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
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                                                                                                                                                                                                                                                                                                                           Example 5; Page 48-49; 93pp; English.
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(YEDA ) YEDA RES & DEV CO LTD.
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AAY71383 standard; protein; 360 AA.
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      The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated Nogo proteins and fragments displaying neurite growth associated. Nogo proteins and fragments displaying neurite growth continuity activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, cependyoma, pinealoma, haemangioblastoma, acoustic neuroma and degenerative nerve diseases e.g. Altheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyporproliferative or benign dysproliferative disorders e.g. psortasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote extructural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The neurons or to promote extructural plasticity of the CNS in disorders where neurite growth, regeneration of maintenance are deficient or desired. The animal medals can be used in disagnostic and screening methods for predisposition to disorders and isagnostic and screening methods for treat or prevent disorders and isagnostic and provent is used in the construction of mutant Nogo-B. The mutant is composed of His-tag/Ty-tag/vector/Nogo-A sequence as 1-171 + mutant is composed of His-tag/Ty-tag/vector/Nogo-A sequence as 1-171 + mutant is composed of His-tag/Ty-tag/vector/Nogo-A sequence as 1-171 + mutant is composed of His-tag/Ty-tag/vector/Nogo-A sequence as 1-171 + mutant is composed of His-tag/Ty-tag/vector/Nogo-A sequence of the mutant second mutant secon
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                                                                                                                                  /note= "Corresponds to residues 975-1162 of rat Nogo A protein shown in AAY71310"
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    17. 171
/note= "Corresponds to residues 1-171 of rat Nogo A protein shown in AAY71310"

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100.0%; Score 175; DB 3;
Best Local Similarity 100.0%; Pred. No. 7.2e-16;
Matches 36; Conservative 0; Mismatches 0;
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                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page; 122pp; English.
                                                                                                                                                                                                                                                                            99WO-US026160
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                                                                                                                                                                                                                                                                                                                                                     (SCHW/) SCHWAB M E. (CHEN/) CHEN M S.
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      Rattus sp.
                                                             Region
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Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiprolliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperprolliferative disorder; benign dysprolliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a rat Nogo B protein which is a potent neural
                                                                                                                                                                                                                                                                                                                                                                                                                             _____Corresponds to amino acids 1-172 of Nogo A protein shown in AAY71310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=""Corresponds to C-terminal 188 amino acids (residues 976-1163) of Nogo A protein (AAY71310). region is common to Nogo A, B and C isoforms" 185. 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .171
note= "Inhibits NIH 3T3 fibroblast spreading"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Protein kinase C (PKC) site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287. .322
/label= Transmembrane domain
/note= "C-terminal hydrophobic :
338. .340
/note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Transmembrane domain
/note= "C-terminal hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Protein kinase C (PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Protein kinase C (PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Protein kinase C (PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Casein kinase II site"
31. .58
/note= "Acidic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268. .270
/note= "Asn is N-glycosylated"
                                                Rat neurite growth inhibitor Nogo B.
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US026160.
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibitory-site
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N-PSDB; ABN86600.

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cell growth inhibitor and is free of all central nervous system (CNS)

myelin material with which it is natively associated. The Nogo B

transcript arises as a result of alternative splicing of Nogo Bene. Nogo

proteins and fragments displaying neurite growth inhibitory activity are

used in the treatment of neoplastic disease of the CNS e.g. glioma,

glioblastoma, medulloblastoma, crantopharyngioma, ependyoma, pincaloma,

haemangioblastoma acoustic neuroma, oligodendroglioma, menagioma,

neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.

Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo

activity can be used to treat or prevent hyperproliferative or benign

cyproliferative disorders e.g. psoriasis and tissue hypertrophy.

Ribozymes or antisense Nogo nucleic acids can be used to inhibit

production of Nogo protein to induce regeneration of neurons or to

promote structural plasticity of the CNS in disorders where neurite

growth, respenzation or maintenance are deficient or desired. The animal

compless and to screen for or test molecules which can treat or

prevent disorders and in diagnostic and screening methods for predisposition

to disorders and to screen for or test molecules which can treat or

prevent disorders or diseases of the CNS. Note: The present sequence is

con given in the specification but is derived from Nogo A protein

sequence (see AAY11385.) which corresponds to residues 1-172 fused to 975

cof Nogo A. The specification claims an alternative version of this

condone sequence (see AAY11385.) which corresponds to residues 1-172 fused to 975

condone sequence (see AAY11385.) which corresponds to residue in claim and sequence in claims an alternative version of this

condone sequence for these SEQ ID numbers in claims and sequence in clude sequences for these SEQ ID numbers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS; central nervous system; tranquillizer; Nogo; vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant; nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; rephrotropic; cytostatic; antigen; gene therapy; neurotransmitter receptor; rat; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mosonego A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

Query Match 100.0%; Score 175; DB 3; Length 360;

Best Local Similarity 100.0%; Pred. No. 7.2e-16;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beserman P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat neurotransmitter receptor protein Nogo-B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB81076 standard; protein; 360 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      981L-00124500.
98WO-US014715.
98US-00218277.
99US-00314161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 360 AA;
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22-DEC-1998;
19-MAY-1999;
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The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering CC combinations in the method is useful for promoting nerve regeneration or its preventing neuronal degeneration in central/peripheral nervous system (NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt from injury/disease, where the injury is spinal cord injury, blunt from injury, paragery such as tumour excision. The disease is not an amages caused by surgery such as tumour excision. The disease is not an ucoimmune disease or neoplasm. The disease results in a degenerative process occurring in either gray or white matter or both. The disease is disease, facial nerve (Bell's) palay, glaucoma, Huntington's choiced, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and disease, acrapal tumnel syndrome, peripheral curpopaths associated with various diseases, including but not limited to uremaia, porphyria, hyposlycemia, Sjorgren Larsson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, bilary dirthosis, primary amyloidosis, obstructive lung diseases, including but not limited syndromes, polybythemia vera, immunoglobulin (19)A- and 199 gamma-complications of various drugs (e.g., metronidazole) and toxins complications of various drugs (e.g., metronidazole) and toxins catternomyloneuropathy, disease, ataxia, amyloid polymenia, perpensionen, p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperpoliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
                                    Promoting nerve regeneration and preventing neuronal degeneration in the central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or analogs/peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternative version of rat neurite growth inhibitor Nogo B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
                                                                                                                                                                           Example 5; Page 47-48; 93pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY71385 standard; protein; 361 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 360 AA;
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The invention relates to a novel isolated gene sequence that is down-
regulated in the spinal cord in response to streptozocin-induced
diabetes, or comprising, hybridising or having at least 80% sequence
identity to a sequence whose expression products are kinases,
phosphateases, in channel proteins, receptors, transporters, G-protein
coupled receptor proteins, DNA-binding proteins, proteases or enzymes,
given in the specification. A gene of the invention has analgesic
cativity, and may have a use in gene therapy. The gene sequences, vector,
compounds for diagnosing or treating pain. The kits are useful for screening of
compounds for diagnosing or treating pain. The kits are useful down-
regulation of a gene sequence in the spinal cord of a mammal in response
composition is useful as a medicament for treating or diagnosing pain.

The present sequence represents a protein encoded by a gene of the
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residues 1-172 fused to 975-1163 of Nogo A. This sequence is an alternative version of the Nogo B sequence (see AAY71383) described in the specification as being residues 1-172 fused to C-terminal 188 amino acids (residues 976-1163) of Nogo A. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID Not. 29 in disclosure of the specification. However the specification does not include sequences for these SEQ ID numbers
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induced diabetes, vector, host cell, animal, polypeptide and antibody, in
screening of compounds for treating or diagnosing pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rat; streptozocin; kinase; phosphatase; ion channel protein; receptor; transporter; G-protein coupled receptor; GPCR; DNA-binding proteins; protease; enzyme; analgesic; gene therapy; pain; diabetes.
                                                                                                                                                                                                                Gaps
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                                                                                                                                                                        Length 361;
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                           288 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 323
                                                                                                                                                                        Match 100.0%; Score 175; DB 3; Local Similarity 100.0%; Pred. No. 7.3e-16; les 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                    1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat foocen-m2 reticulon SEQ ID NO:164.
                                                                                                                                                                                                                                                                                                                                                                                      ADB85283 standard; protein; 379 AA
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07-FEB-2002; 2002GB-00002880.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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N-PSDB; ADB85284.
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                                                                                                                                        Sequence 361 AA;
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                                                                                                                                                                                 Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                       RESULT 7
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Misc-difference 314
                                                                                                 Sequence 403 AA;
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                                                                                                                              Query Match
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                                                                                                                                                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and in the treatment of neoplastic disease of inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, opendyoma, pinealoma, haemangioblastoma, acoustic neuroma, craniopharyngioma, coligodendroglioma, menagiona, neuroblastoma or retinoblastoma and degenerative mich promer Nogo activity can be used to treat or prevent hyporproliferative or benign dysproliferative disorders e.g. plonianial asia and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of meurons or to promote structural plasticity of the CNS in disorders where neurons or to promote structural plasticity of the CNS in disorders where neurons or to prodels can be used in disgnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders and to screen for or test molecules which can be used in disgnostic and screening methods for the construction of mutant BST. The mutant is composed of His-cag/TT-tag/Nogo-A sequence as 760-1162. Nogo A deletion mutants were used for the mapping the inhibitory sites of Nogo Potein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-974, particularly
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                                                                                                                                                                                                                                                                                                 Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative, giltoma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder. Anign dysproliferative disorder; panign dysproliferative disorder; disaps psoriasis; tissue hypertrophy; neuronal regeneration; treatment; agnosis; ptructural plasticity; screening; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
                                                         Gaps
                                                                                                                                                                                                                                                                          Rat Nogo A protein fragment used in the construction of mutant EST.
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                            Length 379;
                                                        Indels
                                                                                                      Match 100.0%; Score 175; DB 7; Local Similarity 100.0%; Pred. No. 7.7e-16; les 36; Conservative 0; Mismatches 0;
                                                                                   1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
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                                                                                                                                                                                        AAY71563 standard; protein; 403
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                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SCHW/) SCHWAB M E. (CHEN/) CHEN M S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schwab ME, Chen MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-400052/34.
 Sequence 379 AA;
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                                                                                                                                                                                                                                                02-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus sp.
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                                                                                                                                                                                                                   AAY71563;
                            Query Match
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amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 313 fibroblast spreading. Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAY1310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative, giltoma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperpoliferative disorder. Alzheimer's disease; Parkinson's disease; psoriasis; tissue hypertrophy; neuronal regenerative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
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11. .238
/note= "C-terminal common region found in Nogo A, B and
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    11. .191
    /note= "Region specifically described in claim 16"

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                                                                                                                                                                                                                     100.0%; Score 175; DB 3; Length 403; 100.0%; Pred. No. 8.2e-16; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                        331 LKFAVLMWVFTYVGALFNGLTLLLLALISLFSIPVI 366
                                                                                                                                                                                                                                                                                                                   1 DKFAVLMWVPTYVGALFNGLTLLILALISLFSIPVI 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Encoded by TAG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat neurite growth inhibitor Nogo C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY71312 standard; protein; 522 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Encoded
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                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 36; Conservative
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Length 522;

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06-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus sp.
                                                                                                                                                                                                                                                                                                           AAY71557;
                                                                                                                                                                                                               RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a rat Nogo C protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) (applin material with which it is natively associated. Nogo proteins and compared the first partial proteins and compared the first partial proteins and compared the first partial first partial proteins and compared to the CNS e.g. glioma, glioblastoma, candiopharyngioma, epondyoma, pincaloma, menagioma, candiophastoma and starting and protein neuroma, oligodendroglioma, menagioma, compared to retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo contivy can be used to treat or prevent hyperproliferative or benign degenerative nerve diseases e.g. postiasis and tissue bypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit conference in the disorders degree e.g. postiasis and tissue or heuron or maintenance are deficient or desired. The animal condels can be used in disagnostic and screening methods for predisposition conference in claim calmin as and screening methods for predisposition or disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID No: 29 in disclosure of the sequences for these SEQ ID numbers for these SEQ ID numbers for these SEQ ID numbers for the contract or include sequences for the contract or the contract or include sequences for the contract or include sequences for the contract or the contract or include sequences for the contract or contract or include sequences for the contract or contract or include sequences for the contract or contract or include sequences for these SEQ ID numbers include sequences for the contract or contract or contract or include sequences for the contract or con
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'note= "Encoded by TAG"
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The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth associated. Nogo proteins and fragments displaying neurite growth control of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative, glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperpoliferative disorder; benjign deproliferative disorder; benjign deproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; diagnosis; ptructural plasticity; screening; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat Nogo A truncated protein used in the construction of mutant Nogo-A.
                                                                                                                    Gaps
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Query Match
100.0%; Score 175; DB 3; Length 5:
Best Local Similarity 100.0%; Pred. No. 1.1e-15;
Matches 36; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                            165 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 200
                                                                                                                                                                                                                           1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY71557 standard; protein; 1162 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-400052/34.
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1089 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 1124
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                                                                                                                              ADS99349;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Regenerating nerves or modulating nerve regeneration comprises inhibiting or modulating p75 signal transduction pathway by administering a transduction agent, e.g. p21 or Rho, or an agent that interacts with the transduction agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a method for regenerating nerves or modulating nerve regeneration. The method involves inhibiting or modulating a p75 signal transduction pathway. The invention is useful for treating, preventing or diagnosing neurological diseases based on nerve regeneration and for identifying agents useful for nerve regeneration. The invention is also useful in gene therapy and for preparing vaccine. The present sequence is the Mus musculus Nogo protein. Note: This sequence is said to encoded by SEQ ID NO 9, however this does not appear
 seent sequence is not given in the specification but is derived from ... Nogo A sequence shown in AAY71310. SEQ ID unubers 35-42 are referred claim 32 and SEQ ID No: 29 in disclosure of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                          Nerve regeneration; gene therapy; vaccine; neuroprotective; nootropic; Nogo; mouse.
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Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                            Match 100.0%; Score 175; DB 3; Length 1162; Local Similarity 100.0%; Pred. No. 2.7e-15; es 36; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                1090 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 1125
                                                                                                                                                                                         1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
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                                                                                                                                                                                                                                                                                                       ADT89537 standard; protein; 1162
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30-APR-2003; 2003US-00427741.
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                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus Nogo protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tohyama M, Yamashita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-698659/68.
N-PSDB; ADT89536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TOHY/) TOHYAMA M.
(YAMA/) YAMASHITA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1162 AA;
                                                                                                  Sequence 1162 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be the same.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus.
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                                                                                                                                Query Match
                                                                  numbers
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Matches
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The invention comprises a composition for regenerating nerves and treating neurological diseases. The composition of the invention contains a PepS Polypeptide and an agent capable of interacting with a Rho GDI, Rho, or Rho kinase polypeptide. The composition of the invention is useful for treating, preventing, disqual cord injury. Or prognosing nervous disease/disorders/conditions, such as: spinal cord injury of the invention and also be used for disrupting or reducing inhibition of the neurite outgrowth or for constructing a network of neurons. In addition, the composition may further be used to identify agents that may treat neurological diseases or induce nerve regeneration. The present amino acid sequence represents a mouse Nogo protein that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition for regenerating nerves or treating neurological diseases comprises a polypeptide (e.g. PepS or PKC) involved in p75 signal transduction pathway, or an agent that interacts with the polypeptide to block the pathway.
                                                                                                                                                                                                                                    nerve regeneration; neurological disease; Pep5; Rho GDI; Rho; Rho kinase; nervous disease; nervous disease; nervous disease; nervous disease; nervous disease; neuron afsorder; prain injury; neurite outgrowth inhibition; neuron network construction; Nogo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Pred. No. 2.7e-15;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INTE-) INTELLECTUAL PROPERTY CONSULTING INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tanaka H, Higuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 10; 613pp; English.
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ID AAY71310 standard; protein; 1163
ADS99349 standard; protein; 1162
                                                                                                                                                                                      Mouse Nogo protein - SEQ ID 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAR-2003; 2003JP-00092923.
30-APR-2003; 2003JP-00125681.
31-JUL-2003; 2003JP-00284559.
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                                                                                                                         (first entry)
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Best Local Similarity 100.0
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamashita T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2004-729217/71.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004087744-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                         30-DEC-2004
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1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36

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and

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The present sequence is a rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. The protein was derived from a cDNA generated by fusing ROl8U37-3, R1-3U21 cDNAs isolated from hexanucleotides-primed rat brain stem/spinal cord library. Mogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, cranlopharyngioma, ependyoma, pinealoma, menagioblastoma, acoustic neuroma, oligodendroglioma, menagiona, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
                                                                                                                                                                                                                                         "C-terminal common region found in Nogo A, B
                                                                                                                                                                              775. 1162
/note= "This region is not essential for inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1090. .1125
/label= Transmembrane_domain
/ore= "C-terminal hydrophobic region specifically
described in claim 16"
                                                                                                                                                                                                                                                                                  988. .1023
/label= Transmembrane_domain
chcs= "C-terminal hydrophobic region specifically
described in claim 16"
                                                                                                                   /note= "PKC and casein kinase II sites"
956
                                                                                                                                                           'note= "PKC and casein kinase II sites"
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/note= "Protein kinase C (PKC) site"
393
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1089
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                                     "Protein kinase C (PKC)
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                                                     312. .914
Monte= "Asm is N-glycosylated"
225. 927
Mote= "Asm is N-glycosylated"
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note= "Asn is N-glycosylated"
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'note= "Asn is N-glycosylated"
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/note= "C-t
isoforms"
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                                          notes
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N-PSDB; AAD01173.
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              Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; giltoma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperpoliferative disorder. benign dysproliferative disorder; benign dysproliferative disorder; dispessionsis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening.
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                                                                                                                                                                                                                                                                                                                                                                                                         "Region specifically described in claim 16"
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note= "used as immunogen to generate antibody
                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .171
/note= "Inhibits NIH 3T3 fibroblast spreading"
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68. .470
note= "Asn is N-glycosylated"
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502
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/note= "Casein kinase II site"
868
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note= "Asn is N-glycosylated"
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note= "Asn is N-glycosylated"
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e= "Acidic region"
                                                                                         Rat neurite growth inhibitor Nogo A.
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542. .722
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activity"
                                                             (first entry)
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/note= "...
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//note= "Casein kinase II site"
762. .1163
/note= "used as immunogen to generate antibody AS Bruna"
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623. .640
/note= "used as immunogen to generate antibody AS 472"
                                  /label= Unknown
/noce= "There I Lys at this position in the sequence
/hoce= "AAX71310"
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shown in AAX71310"
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note= "C-terminal common region found in Nogo A, B
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note= "C-terminal hydrophobic region"
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/labble Transmembrane domain
//notes "C-terminal hydrophobic region"
1141. .1143
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855
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868
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/notes "Men is N-glycosylated"
125. 927
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'note= "Asn is N-glycosylated"
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/note= "Asn is N-glycosylated"
    'note= "Asn is N-glycosylated"
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/label= Tra
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542. .722
576
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        Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce responsation of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for prediaposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence designated as SEQ ID No: 2 is stated to be the same as the sequence in Fig. 13 (see ANY1384) of the specification. However, this sequence does not match the sequence given in Fig. 13. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID No: 29 in disclosure of the secuence for the specification does not include sequences for the specification does not include sequences for the secuence of the secuence of the secuence for the secuenc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
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horte= "There is Leu at this position in the sequence
shown in AAY71310"
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/note= "This region is not essential for inhibitory
activity"
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note= "Inhibits NIH 3T3 fibroblast spreading"
                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 175; DB 3; Length 1163; Best Local Similarity 100.0%; Pred. No. 2.7e-15; Matches 36; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alternative version of rat neurite growth inhibitor Nogo A.
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                                                                                                                                                                                                                                                                                                                                                                            1090 LKPAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 1125
                                                                                                                                                                                                                                                                                                                                                       1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Casein kinase II site"
31. .58
/note= "Acidic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY71384 standard; protein; 1163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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468. .470
                                                                                                                                                                                                                these SEQ ID numbers
                                                                                                                                                                                                                                                   Sequence 1163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Inhibitory-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY71384;
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sequence

U and neurotransmitter receptor; rat; receptor.

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Search completed: February 17, 2006, 03:49:30 Job time : 169.444 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is an alternative version of rat Nogo A protein
which is a potent neural cell growth inhibitor and is free of all central
nervous system (GNS) myelin material with which it is natively
associated. Nogo proteins and fragments displaying neurite growth
associated. Nogo proteins and fragments displaying neurite growth
inhibitory activity are used in the treatment of neoplastic disease of
the CNS e.g. glioma, glioblastoma, meduloblastoma, craniopharyngioma,
cligodendroglioma, menagioma, meturoblastoma and
egenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
Therapeutics which promore Nogo activity can be used to treat or prevent
hyperproliferative or benigh dysproliferative disorders e.g. psoriabis
and tissue hypertrophy. Ribozymes or antisense Nogo mucleic acids can be
used to inhibit production of Nogo protein to induce regeneration of
neurons or to promote structural plasticity of the CNS in disorders where
cuert or promote structural plasticity of the CNS in disorders where
neurite growth, regeneration or maintenance are deficient or desired.
The canimal models can be used in disgnostic and screening methods for
treat or prevent disorders and to screen for or treat conference shown in Pig.
The profession of the profession of the Nogo A sequence shown in Pig.
The AMY13101 SEQ ID numbers 35-42 are referred in claim 32 and SEQ
Oses not include sequences for these SEQ ID numbers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                   Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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llarity 100.0%; Pred. No. 2.7e-15;
Conservative 0; Mismatches 0; Indels
                                          /note= "Protein kinase C (PKC) site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Asn is N-glycosylated"
1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat neurotransmitter receptor protein Nogo-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB81074 standard; protein; 1163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Fig 13; 122pp; English.
                                                                                                                                                           99WO-US026160
                                                                                                                                                                                               98US-0107446P.
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                                                                                                                                                                                                                                                                                                Chen MS;
                                                                                                                                                                                                                                                                                                                                    WPI; 2000-400052/34.
                                                                                                                                                                                                                                   (SCHW/) SCHWAB M E. (CHEN/) CHEN M S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 36; Conserv
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                                                                                 WO200031235-A2
                           Modified-site
                                                                                                                                                           05-NOV-1999;
                                                                                                                                                                                                 06-NOV-1998;
                                                                                                                       02-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB81074;
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Matches
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The invention relates to promoting nerve regeneration or conferring neuropactection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering central/peripheral nervous system (NS) The method involves administering nervertable according to the analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt from injury/disease, where the injury is spinal cord injury, blunt from injury/disease, where the injury is spinal cord injury, blunt from injury/disease, where the injury is spinal cord injury, blunt from injury/disease, where the injury is spinal cord injury, blunt from injury/disease, where the injury is spinal cord injury, blunt from injury/disease is not an autoimmume disease or neoplasm. The disease is not an autoimmume disease or neoplasm. The disease is not an autoimmume disease or neoplasm. The disease is not an autoimmume disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and cyleases, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, as Creutzfeldt-Jakob disease, capal tunnel syndrome, paripheral curopathy, chronic ataxic neuropathy, bilary cirrhosis, primary anyloidosis opphyria, hypoglycemia, Sjorgren Larsson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, bilary cirrhosis, primary amyloidosis, obstructive lung diseases, accomegaly, malebsorption syndromes, polycythemia vera, immunoglobulin (Ig)A- and 1gG gamma compathies, complications of various drugs (e.g., metronidazole) and toxins carnomyclomeuropathy, distant axonal neuropathy, sequence represents the rat carnomyclomeuropathy and present sequence represents the rat controcrean entergence or lipoproteinemia. The present sequence represents the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Promoting nerve regeneration and preventing neuronal degeneration in the central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or analogs/peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cohen IR, Beserman P, Mosonego A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hauben E,
                                                                                                                                                                                                                                                                                               98IL-00124500.
98WO-US014715.
98US-00218277.
99US-00314161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                              28-JUN-2001; 2001US-00893348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eisenbach-Schwartz M,
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N-PSDB; ABN86600.
Rattus norvegicus.
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                                                                          US2002072493-A1.
                                                                                                                                                                                                                                                                                                                                                  21-JUL-1998;
22-DEC-1998;
19-MAY-1999;
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                                                                                                                                                    13-JUN-2002.
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Best Local S
Matches 36
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Pebruary 17, 2006, 03:49:55; Search time 25.7778 Seconds (without alignments) 11, 12, 13, 1111no cell updates/sec Run on:

US-09-830-972A-2_COPY_1090_1125 175 1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	neuroendocrine-spe	tropomyosin-relate	neuroendocrine-spe				othetica	B. subtilis YoaT p	ж.	hypothetical prote	hypothetical prote	hypothetical prote	probable membrane	Na+-transporting t	hypothetical prote	hypothetical prote	probable membrane	probable glucose t	cation-efflux syst	hypothetical prote	cytochrome D ubiqu				hypothetical prote	amino acid ABC tra	hypothetical prote	0	hypothetical prote
	OI	160904	A60021	A46583	T26213	T26216	T26215	T05595	AD1561	AE1204	T13013	E84899	A84527	AI0142	S12619	D71112	F89780	AG0337	T43657	T44365	G90008	G72119	H86503	B64815	A85587	H90736	H95174	B98041	S26018	AI2278
	DB	~	N	~	~	~	7	7	N	7	~	~	0	~	7	~	7	7	~	~	N	~	~	-	~	~	~	~	н	N
	Query Match Length 1	208	267	116	222	2484	2607	275	267	267	271	255	183	236	289	413	449	220	557	325	325	344	344	234	234	234	213	232	281	91
de	Query Match	85.7	85.7	85.7	55.4	55.4	55.4	43.7	42.6	40.3	38.9	37.7	35.4	35.1	34.9	34.0	33.7	33.4	32.6	32.0	32.0	32.0	32.0	31.7	31.7	31.7	30.9	30.9	30.9	30.6
	Score	150	150	150	97	97	97	76.5	74.5	70.5	68	99	62	61.5	61	59.5	59	58.5	57	26	26	26	26	55.5	55.5	55.5	54	54	54	53.5
	Result No.		7	ю	4	2	9	7	80	O	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	26	27	28	29

conserved hypothet proton/sodium-glut	permease homolog y hypothetical prote	spore germination	hypothetical prote	sodium-galactoside	hypothetical prote hypothetical prote	NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas	-bi	dedA protein - Esc	hypothetical prote
B82383 D84127	D70035 H75055	H83891	E90540	H87465	B85016 D95302	T17175	T17178	T17181	H83243	XMECAD	B85873
70	70	100	N 19	~	n n	~	7	~	7	Н	7
240	520	373	507	514	242 268	459	459	459	610	219	219
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30.3	30.3	30.0	30.0	30.0	29.7	29.7	29.7	29.7	29.7	29.4	29.4
53 30.3 53 30.3		52.5 30.0			52 29.7	52 29.7	52 29.7	52 29.7	52 29.7	•	51.5 29.4

ALIGNMENTS

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neuroendocrine-specific protein C - human clister change 09-Jul-2004 clispecies: Homo sapiens (man)
Clate: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
Clacession: 160904
Clacession: 160904
Jul 1800. Chem. 268, 13439-13447, 1993
Jul 1810. Chem. 268, 13439-13447, 1993
Jul 1810. Chem. 268, 13439-13447, 1993
Jul 1810. Chem. 268, 13439-13447, 1993
Alitical Cloning and expression of alternative transcripts of a novel neuroendocrine-spectal control of alternative transcripts of a novel neuroendocrine-spectal control of alternative translated from GB/EMBL/DDBJ
Alitical type: mRNA
Alitical control of alternative translated from GB/EMBL/DDBJ
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85.7%; Score 150; DB 2; Length 20
Best Local Similarity 72.2%; Pred. No. 9.5e-11;
Matches 26; Conservative 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: GDB.RTN1; NSP
A;Cross-references: GDB:203968; OMIM:600865
A;Map position: 14q21-14q22
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RESULT 2 A60021

coveryonyosin-related protein, neuronal - rat
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A6021
Brain Res. Mol. Brain Res. 10, 33-41, 1991
Brain Res. Mol. Brain Res. 10, 33-41, 1991
Brain Res. Mol. Brain Res. 10, 33-41, 1991
A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue.
A;Teference number: A60021; MUID:91278684; PMID:1647480
A;Accession: A60021
A;Nolecule type: mRNA
A;Residues: 1.267 - 481Es
A;Cross-references: UNIPARC:UPI0000086535; EMBL:X52817; NID:9456549; PIDN:CAA37001.1; PII
C;Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropon

Gaps ö Length 267; Score 150; DB 2; Length 267 Pred. No. 1.2e-10; 9; Mismatches 1; Indels Query Match 85.7%; Best Local Similarity 72.2%; Matches 26; Conservative

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1 LKEAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36

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Query Match
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Matches 15
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Adebada

natureendocrine-specific protein, splice form A - human

N;Contains: neuroendocrine-specific protein, splice form B

N;Contains: neuroendocrine-specific protein, splice form B

N;Contains: neuroendocrine-specific protein, splice form B

C;Species: Home sapiens

(man)

C;Species: Home sapiens

(man)

C;Species: Home sapiens

(man)

C;Species: 124-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004

C;Accession: Ad6583 # 160903

A;Trile: Cloning and expression of alternative transcripts of a novel neuroendocrine-species parallely preliminary; translated from GB/EMBL/DDBJ

A;Reference number: Ad6583 # WID:93293865; PMID:7685762

A;Accession: Ad6583

A;Accession: Ad6583

A;Accession: 16090

A;Access
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A;Experimental source: clone W06A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26216
Q;Ainscough, R.
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C,Species: Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C,Accession: T26213
R,Ainscough, R.
Submitted to the EMBL Data Library, August 1996
A,Reference number: 220173
A,Accession: T26217
A,Molecule type: DNA
A,Nolecule type: DNA
A,Residues: 1-222 Wills
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A; Map position: 14q21-14q22
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A;Map position: 5
A;Introns: 27/1; 77/2; 201/2
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hypothetical protein F9D16.100 - Arabidopsis thaliana hypothetical protein F9D16.100 - Arabidopsis thaliana (mouse-ear cress)

Lypothes: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

CjSecsesion: 1005595

R.Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.)

R.Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.)

A.; Reference mumber: 215419

A.; A.; Reference mumber: 215419

A.; Molecule type: DNA

A.; Molecule type: DNA

A.; Cross-references: UNIPROT: Q9SUR3; UNIPARC: UPIO0000AB22F; EMBL: AL035394

A.; Cross-references: UNIPROT: Columbia; BAC clone F9D16
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Hypothetical protein WOGA7.3a - Caenorhabditis elegans

Hypothetical protein WOGA7.3a - Caenorhabditis elegans

Cippedies: Caenorhabditis elegans

Cippedies: 15-00ct-1999 #text_change 09-Jul-2004

Cipcesion: T26215

Ryainscough, R.

Submitted to the EMBL Data Library, August 1996

A;Reference number: Z2017

A;Reference number: Z2017

A;Reference number: T26312

A;Reference number: T26312

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;References: UNIPPAC:UPI000007623E; EMBL:Z78066; PIDN:CAB01522.2;

A;Cross-references: UNIPPAC:UPI000007623E; EMBL:Z78066; PIDN:CAB01522.2;

A;Experimental source: clone WOGA7
submitted to the EMBL Data Library, August 1996
A,Reference number: Z20173
A,Accession: T26216
A,Estuts: pre-failminary; translated from GB/EMBL/DDBJ
A,Rolecule type: DNA
A,Role
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A.Genetics:
A.Gene: CESP.WGAT.3a
A.Map position: 5
A.Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2
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2526 IKFGLVLWSLTYIASWFSGFTLAILGLLGVFSVPKV 2561
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A;Introns: 89/1; 149/2; 196/3; 220/1
A;Note: F9D16.100
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hypotherical protein At2946170 [imported] - Arabidopsis thaliana hypotherical protein At2946170 [imported] - Arabidopsis thaliana (mouse-ear cress) (c;5pecte Arabidopsis thaliana (c;6pecte Arabidopsis Arabidopsis (c;6pecte Arabidopsis Arabidopsis (c;7pecte Arabidopsis Arabidopsis (c;7pecte Ar
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A4625.7
A4625.2
A4625.2
A5poches: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Arabidopsis thaliana (mouse-ear cress)
C; Arabidopsis thaliana (mouse-ear cress)
B; Lin, X; Raul, Si; Rounsley, S.D.; Shea, T.P.; Bentco, M.I.; Town, C.D.; Fujii, C.Y.; N
B; Lin, X; Raul, Si; Rounsley, S.D.; Shea, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Niedman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
N; Ttle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID: 20083487; PMID: 10617197
A; Status: profilminary
A; Rocession: A84527
A; Status: profilminary
A; Rocession: A84527
A; Residues: T183 <STO>
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hypothetical protein F8L21.10 - Arabidopsis thaliana Gispecies Arabidopsis thaliana (mouse-ear cress) Gispecies Talogis Basquence Tavision 13-Aug. 1999 Hext_change to the Protein Sequence Database, July 1999 Aircession: T101013 Aircession: T101013 Aircession: T101013 Aircession: T101013 Aircession: T101014 Ai
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174 LMVVVGLMIISVVGNWFNFLFLVXICFVILHTVPML 209
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A;Map position: 4
A;Introns: 85/1; 145/2; 192/3; 216/1
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Best Local S:
Matches 11
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, C; Accession: ABL204
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Jones, L.M.; Karst, U.
Science 284, R49-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; MaAuthors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: ABl077; MUID:21537279; PMID:11679669
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Rocession: Buchaid, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.D.; Donninguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.D.; Donninguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, G.; Madueno, E.; Maitournam, A.; Ma A, Authors: Kreft, J.; Kunn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A, A, Hille. Comparative genomics of Listeria species.
A, Pittle. Comparative genomics of Listeria species.
A, Pittle. Comparative genomics of Listeria species.
A, Fatus: preliminary
A, Rocession: All 561
A, Status: preliminary
A, Rocession: All 561
A, Residues: 1-567 cGLA
A, Residues: 1-567 cGLA
A, Cross-references: UNIPROT: Q92CZZ; UNIPARC: UPI00000CC4ZE; GB: ALS9202Z; FIDN: CAC9626O.1;
A, Experimental source: strain Clipil262
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A;Experimental source: strain EGD-e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 12-Jul-2004
C;Accession: AD1561
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Pred. No. 0.29;
6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 42.6%; Score 74.5; DB 2; Length 267; Local Similarity 46.2%; Pred. No. 0.098; nes 18; Conservative 5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKFFRLLWVFTWKQALCCLFPGIIFISLALTKLIBIPFI 39
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                                                                                                                                                                                         KFAVL---MWVFTYVGALFNGLTLLILALISLFSIPV 35
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Local Similarity 43.6%;
les 17; Conservative
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C;Superfamily: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: lin102>
C;Superfamily: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-267 < GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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probable membrane protein YPO1163 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: A10142
R;Parkhill, J; Wren, B.W.; Thomson, Nr.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
R;Parkhill, J; Wren, B.W.; Thomson, Nr.; Titball, R.W.; Davis, P.; Dougan, G.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Stevens, K.; Whitehead, S.; Barrell,
il, M.; Rutherford, K.; Simmonds, M.; Stelton, J.; Stevens, K.; Whitehead, S.; Barrell,
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Reterence number: AB0001; MUID:21470413; PMID:11586360
A;Reterence number: AB0001; MUID:21470413; PMID:11586360
A;Reterence number: AB0001; MUID:21470413; PMID:11586360
A;Reterence: UNIPROT:Q8ZGWI; UNIPARC:UPI00000DCAIF; GB:AL590842; PIDN:CAC90004.1;
C;Gene:Textics:
A;Gene: YPO1163
A;Scherichia: A;Gene: YPO1163
A;Superfamily: Escherichia coli ybhL protein
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A;Status: translation not shown
A;Nolecule type: DNA
A;Rolecule type: DNA
A;Rosidues: 1-113. 17, 115-289 <ESS>
A;Ross-references: UNIPARC:UPT000016FD91; EMBL:X53960; NID:g45643; PIDN:CAA37911.1; PID
B;Krunholz, L.R.; Bser, U.; 34, 24, 192
A;Title: Characterization of the genes coding for the F(1)F(0) subunits of the sodium de
A;Reference number: S29034
A;Accession: S29035
A;Molecule type: DNA
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## Secidues: 1-289 CKAI>

| Cross-references: Univery: P21903; UNIPARC: UPI000012632F; EMBL: X54809; NID: g45607; PIDN

| EBSet, U.; Krumholz, L.R.; Simoni, R.D.

| EBSet, U.; Krumholz, L.R.; Simoni, R.D.

| EBSet, U.; Krumholz, L.R.; Simoni, R.D.

| First Reference of the F(0) subunits of the sodium dependent F(1)F(0) ATPAS

| PREFerence number: S12611; MUID: 91016937; PMID: 2170948
A, Cross-references: UNIPROT: Q98HU8; UNIPARC: UP100000A63C8; GB: AE002093; NID: 94662633; PI
C; Genetics:
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                                                                                                                                                                                         Query Match 35.4%; Score 62; DB 2; Length 183; Best Local Similarity 31.4%; Pred. No. 2.1; Matches 11; Conservative 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                   103 RVSVVLMTVSFVGNFLNFLTILXLGVVLSLLIPFL 137
                                                                                                                                                                                                                                                                                                                                      2 KFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.1%; Score 61.5; D
Local Similarity 63.6%; Pred. No. 3;
les 14; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 LKSPALMWVVTYIGVLVFVGLT 184
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                                                                                                   A;Gene: At2g15280
A;Map position: 2
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DV1112

bypothetical protein PH0667 - Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Species: 14-Aug.1998 #sequence_revision 14-Aug.1998 #text_change 12-Jul-2004

C;Accession: D71112

Sawada, M.; Horikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
R;Kawarabayasi, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
M.; Ohiku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. S, 55-76, 1998

A;Tatle: Complete sequence and gene organization of the genome of a hyper-thermophilic as
A;Reference number: A71000; WUID:98344137; PMID:9679194

A;Recession: D7112

A;Rediuse: I-413 - KAMP

A;Residuse: I-413 - KAMP

A;Residuse: Lype: DNA

A;Residuse: Lals - KAMP

A;Residuse: 
A;Residues: 1-113,'I',115-287 <KRU1>
A;Cross-references: UNIPARC:UPI0000175ED5; EMBL:X58461
R;Crumholz. L.R.
B;Krumholz. L.R.
B;Krumholz. L.R.
A;Reference number: S23333
A;Accession: S23334
A;Molecule type: DNA
A;Residues: 1-13,'I',115-289 <KRU2>
A;Residues: 1-13,'I',115-289 <KRU2>
A;Rosidues: UNIPARC:UPI000016FD31; EMBL:X58461; NID:g897797; PIDN:CAA41368.1; PII
B;Kraim G; Ludwig, W; Dimroth, P; Schleifer, K.H.
B;Kraim G; Ludwig, W; Dimroth, P; Schleifer, K.H.
A;Reference number: S24366; MUID:9239434; PMID:1386022
A;Title: Cloning, sequencing and in vivo expression of genes encoding the P(0) part of th
A;Reference number: S24367
A;Molecule type: DNA
A;Residues: 1-95,'L',97-157,'T',158-205,'L',207-224,'P',226-289 <KRW>
A;Cross-references: UNIPARC:UPI0000175ED6; EMBL:X66102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-289 <LUD>
A;Cross-references: UNIPARC:UP1000012632F; EMBL:X66102; NID:945599; PIDN:CAA46894.1; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: uncB
S.Superfamily: H(+)-transporting ATP synthase protein 6
C.Keywords: ATP biosynthesis; blocked amino end; hydrolase; membrane-associated complex;
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Local Similarity 56.0%; Pred. No. 4.1;
ies 14; Conservative 3; Mismatches 6; Indels
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Best Local Similarity 38.7%; Pred. No. 8.5;
Matches 12; Conservative 10; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Ludwig, W. Submitted to the EMBL Data Library, May 1992 A;Reference number: S36000 A;Accession: S36000.
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RTN4 MOUSE STANDARD; PRT; 199 AA.

AC Q99P72; Q9CTE3;
DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last sequence update)
  Q7L7QC_HUMAN
Q56B1G_HUMAN
Q4 PZ80_XENTR
C6RSSB_CH1CK
Q81UA4_HUMAN
Q5NAJO_CH1CK
RTR4_HUMAN
Q5NAJO_CH1CK
RTR4_HUMAN
Q5JRV6_XENLA
Q6JRV6_XENLA
Q5JRV6_XENLA
Q5JRW3_XENLA
Q5JRW3_XENLA
Q5JRW3_XENLA
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       Q99p72 mus musculu Q78bb78 mus musculu Q8bb78 mus musculu Q8k397 mus musculu Q6k131 rattus norv Q8bb45 mus musculu Q8bc95 mus musculu Q8bc96 mus musculu Q8bc96 mus musculu Q8bc97 mus musculu Q6bc97 mus musculu Q6c15 musculu G6c15 mus musculu Q6c19 mus musculu Q6c10 musuus musculu 
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(without alignments)
154.453 Million cell updates/sec
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                                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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175
1 LKPAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                    2166443 segs, 705528306 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTN4 MOUSE

O'08N51 MOUSE

ORBH78 MOUSE

ORSTS7 MOUSE

ORSTS7 MOUSE

OSACH RAT

OSBERY MOUSE

OSACH RAT

OSBERY MOUSE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                            score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                    Run on:
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T E	28-FEB-2003 (Rel. 41, Labt Bequelice update)
Z C	Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
G S	Name=Rtn4; Synonyms=Nogo;
SO	Mus musculus (Mouse)
8	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
ပ	Mammalia, Butheria, Buarchontoglires, Glires, Kodentia, Sciurognaciii,
ဗ	Muroidea; Muridae; Murinae; Mus.
ŏ	NCBI_TaxID=10090;
RN	(1)
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=3T3-L1; TISSUE=Adipocyte;
B	Coulson A.C., Craggs P.D., Morris N.J.;
RT	"Mouse vp20/RTN4C cDNA.";
RL	Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN	[2]
RP	NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] OF 170-199.
RC	STRAIN=C57BL/6J; TISSUE=Embryo;
RX	MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA	Nikaldo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
A'A	Yadi K., Tomaru Y., Haseqawa Y., Nogami A., Schonbach C., Gojobori T.,
A A	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
d d	Schriml I. M. Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
e c	Blake I A Bradt D Brusic V. Chothia C., Corbani L.E., Cousins S.,
5 6	nalls w Dragani T A Pletcher C.F. Forrest A. Frazer K.S.,
5 6	Dalla B., Dragami in., inc., inc., in., in., in., in., in., in., in., in
5 8	deabletiand 1. definition of direction of deabletiand of deabletia
5 6	GILIMICAL O., GUELLICICA O., GILLOCALLA V. KACIALERRI R.M., KING B.L.,
5 ;	Maida A., Nawaji A., Marabawa I., Morabawa I., Morabawa I., Marabawa I
\$;	Konagaya A., Kurochikin 1.V., Lee I., Louisia J., John H.
ş	MAGIOCE D.K., MAICAIB D., MAICAID T., MAICAID C., MAICAID C.
R.	Nagashima T., Numata K., Okido T., Pavan W.J., Ferces G.,
æ	Petrovsky N., Pillai R., Pontius J.U., Qi D., Kamachanian 3.,
RA RA	Ravasi T., Reed J.C., Reed D.J., Reid J., King B.Z., Kingwald M.,
RA	Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
R	Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
R3	Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
R.	Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA	Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA.	Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA	Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA	Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA	Mivazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
R.	Yasunishi A., Yoshino M., Waterston R., Lander B.S., Rogers J.,
RA	Birnev E., Havashizaki Y.;
RT	"Analysis of the mouse transcriptome based on functional annotation of
RT	60,770 full-length cDNAs.";
RL	Nature 420:563-573 (2002).
ខ	-i- FUNCTION: Potent neurite outgrowth inhibitor which may also help
,	

33098443310 33098443310 330987443310 330987443310

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STRAIN-129/SVC377, and 129SVC37; DOI=10.1016/S0022-2836(02)01179-8; MEDLINE-23976540; PubMed=124888097; DOI=10.1016/S0022-2836(02)01179-8; MEDLINE-23976540; PubMed=124888097; DOI=10.1016/S0022-2836(02)01179-8; MEDLINE-23976540; PubMed=124888097; DOI=10.1016/S0022-2836(02)01179-8; MEDLINE-23976540; PubMed=12488097; ALL STRAIN-12488097; MEDLING-10.1016/S0022-2836(02)01179-8; MEDLING-10.1016/S002-2836(02)011
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8; Oertle T., Huber C., van der Putten H., Schwab M.E.; "Genomic structure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTN4 (Reticulon 4).
Musmeskuta, ORKnamesRp23-1760S.4-007;
Musmesulus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Sciurognathi;
Muridae; Murinae; Mus.
MUSDI_TAXID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 100.0%; Score 175; DB 2; Length 199; Local Similarity 100.0%; Pred. No. 4.9e-12; hes 36; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=1298vcJ7;
Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [4]

NUCLEOTIDE SEQUENCE.

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NUCLEOTIDE SEQUENCE.

NUCLEOTIC SEGUENCE.

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                                                                                                                                                                                                                                                                                                                                [3]
NUCLEOTIDE SEQUENCE.
NUCLEAIN=129/SvoJ7;
Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                      STRAIN-129SvcJ7;
Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBH78; OBH78; ORLIMINARY; PRT; 356 AA.
QBH78; OBH78; ORLIMINARY; Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
10-MAY-2005 (TrEMBLrel. 33, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 LKFAVLMWVFTYVGALFNGLTLIILALISLFSIPVI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
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J. Mol. Biol. 325:299-323 (2003).
                                                                                                      human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003).
GLEGOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
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Matches
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Q8BH78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LO-MAX-2005 (TrEMBLrel. 30, Created)
10-MAX-2005 (TrEMBLrel. 30, Last sequence update)
Name-Rtn4; ORFNames-ERP23-17605.4-009;
Mus musculus (Mouse).
Enkaryotasi Metazoa; Chordata; Caniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
(11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the regeneration of the nervous central system in adults (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                   SUBDANT:
Binds to RINAR. Interacts with Bcl-xl and Bcl-2 (By SIUBDANT:
Binds to RINAR. Integral membrane protein. Anchored to the SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the membrane of the endoplasmic reticulum through 2 putative transmembrane domains (By similarity).
ALTERNATIVE PRODUCTS:
Byent-Alternative splicing; Named isoforms=1;
Comment=Alternative splicing; many be produced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic (Potential).
Reticulon.
07BESD580059ED9C CRC64;
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                                                                                                                                                                                                                                                                                                                                                      Name=1;
IsoId=Q99P72-1; Sequence=Displayed;
SIMILARITY: Contains 1 reticulon domain.
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NUCLEOTIDE SEQUENCE.
STRAIN=129SvcJ7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 162 PO
163 199 CYI
12 199 Rei
199 AA; 22466 MW;
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TRANSMEM
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NUCLECTIDE SEQUENCE.

TISSUES-LANG, and Placenta;

TISSUES-LANG, and Placenta;

TISSUES-LANG, and Placenta;

XS strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XR strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI stansper R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.L., Wang J., Haish F.F.,

And Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Haish F.F.,

And Sarks M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Tochiquki S., Carninci P., Prange C.,

Brownstein M.J., Uddin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Robert S.A., McEwan P.J., McRernan K.J., Malek J.A., Gluber R.A.,

Richards S., Worley K.C., Hala S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hala S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Mala S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marza M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marza M.A.,

Schnerch A., Schein J.E., M., Karta M.A.,

Schnerch A., Schein J.E., M., Marza M.A.,

Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Murinae, Murinae, Rattus.
NCBI_TAXID=10116,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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MEDLINE-22715897; PubMed-12832288;
OSTTLE T., Klinger M., Stuermer C.A., Schwab M.E.;
A reticular rhapsody; phylogenic evolution and nomenclature of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venus.

VENUS.

10-MAR-2003 (TERMELrel. 23, Last sequence update)

10-MAR-2003 (TERMELrel. 23, Last sequence update)

10-MAR-2003 (TERMELrel. 30, Last annotation update)

NAME-Straf, ORFNames-RP23-17605.4-006;

Mus musculla (Mouse)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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NOTE MAC PROJECT AND SEQUENCES AND SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA seguences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Match 100.0%; Score 175; DB 2; Local Similarity 100.0%; Pred. No. 7.6e-12; Nes 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
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FASEB J. 17:1238-1247(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBBHFS MOUSE PRELIMINARY;
QBBHFS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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08BHFS_MOUSE
00BHFS_MOUSE
AC 08BHFS_7
DT 01-MAR-20
DT 10-MAR-20
DE RTW4 (Ref
CN Name-Rtri4

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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A Jin W., Li R., Long M., Shen J., Ju G.;

A Jin W., Li R., Long M., Shen J., Ju G.;

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

R MG1, MG11193133, AAM77069.1; -; mRNA.

R GO, GO:0042025; C:cell projection; IDA.

R GO, GO:0043025; C:cell projection; IDA.

R GO, GO:0005713; F:protein binding; IPI.

DR GO, GO:000125; P:protein binding; IPI.

CO, GO:000125; P:protein binding; IPI.

DR GO, GO:000125; Reticulan.

DR HEREP, PROSA15; Reticulan.

DR Ffam; PPO245; Reticulan; 1.

DR PROSITE; PS50845; RETICULON; 1.
                                                                                MGI; MGI:1918835; Rtn4.

GO; GO:0042955; C:cell soma; IDA.

GO; GO:0042955; C:cell soma; IDA.

GO; GO:0005783; C:celd soma; IDA.

GO; GO:0005783; C:endeplesmic reticulum; IDA.

GO; GO:0001555; P:proctein binding; IPI.

GO; GO:0001555; P:angiogenesis; IMP.

GO; GO:0001555; P:angiogenesis; IMP.

GO; GO:0001855; Reticulon.

RerePro; IPRO0388; Reticulon.

Pfam; PF02453; Reticulon; 1.

RESSITE; PS56845; RETICULON; 1.

SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 7.5e-12;
Matches 36; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBK3G7_MOUSE PRELIMINARY;
Q8K3G7;
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NUCLEOTIDE SEQUENCE.
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Name=Rtn4;
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ORAGO MOUSE

AC ORAGOT /
DIT 01-OCT-2/
DT 01-OCT-2/
DT 01-MAR-2/
DT 01-OCT-2/
DT 01-MAR-2/
DT 01-DCT-2/
DT 01-DC
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QGIRL3 RAT
10 GGIRL3
AC GGIRL3
DT 05-JUL
DT 13-SEP
DE Rtn4 p
GN Name=RR
GN Name=RC
C BUKATY
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Length 379;

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Match 100.0%; Score 175; DB 2;
Local Similarity 100.0%; Pred. No. 7.8e-12;
Les 36; Conservative 0; Mismatches 0;
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Name=Rtn4;
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                                                                                                                      NUCLECTIDE SEQUENCE.
STRAIN=129/SvcJ7, and 1298vcJ7;
STRAIN=129/SvcJ7, and 1298vcJ7;
MEDLINE=223/6540; bubmed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
Oertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bumanlai, Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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MEDLINE2271589; PubMed=12832288;
MEDLINE22715897; PubMed=12832288;
OerLie T., Klinger M., Stuermer C.A., Schwab M.E.;
M. reticular rhapsody: phylogenic evolution and nomenclature of the RTN/Knogo gene family. The Factor of the Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-1295vcJ7;
Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                        STRAIN=129/SvcJ7;
san der Putten H.;
Submitteed (MAY-2002) to the EMBL/GenBank/DDBJ databases
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13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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100.0%; Score 175; DB 2;
Best Local Similarity 100.0%; Pred. No. 7.8e-12;
Matches 36; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                               human and mouse nogo/rtn4.";
J. Mol. Biol. 325:299-323(2003).
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murimae; Mus.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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C3; MEDINE-21380257, PubMed=12477932, DOI=10.1073/pnas.242603899; MEDINE-213802577, PubMed=12477932, DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altechul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.K.
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| VUCLEOTIDE SEQUENCE. |
| VOCACIO SECUENCE. |
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08K290, MOUSE PRELIMINARY; Created)
01-CCT-2002 (TERMILE1. 22, Created)
01-CCT-2004 (TERMILE1. 22, Last sequence update)
01-MAR-2004 (TERMILE1. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBOWSE MOUSE PRELIMINARY; PRT; 578 AA.
QBOWSE;
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                                                                                                                                                                                                                                                       306 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 341
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., R. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rahaa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Rohas S.A., McKernen K.J., Malek J.A., Gunzarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hy Fahey J., Helton E., Ketteman M., Rodrigues S., Sanchez A., Matting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blatesiey R.W., Touchmon J.W., Schen E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length human moven by the superces "."
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WOLEOTIDE SEQUENCE.
STRAIN=129/SvcJ7, and 1285vcJ7;
MEDLINE=129/SvcJ7, and 1285vcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
Oertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTION OF THE MANAGE PRELIMINARY; PRT; 1046 AA.

OBBGK77

OBBGK77

OBBGK77

OL-MAR-2003 (TREMBLrel. 23, Last sequence update)

OL-MAR-2003 (TREMBLrel. 23, Last sequence update)

OL-MAR-2005 (TREMBLrel. 30, Last annotation update)

RTN4 (Reticulon 4).

RTN4 (Reticulon 4).

Mane=Rtn4, ORRHames=RP23-17605.4-008;

Nus musculus (Mouse).

Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Enkaryota; Mariala; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

Muridae; Murinee; Mus.

ORRETTAXID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
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L Local Similarity 100.um
Thes 36; Conservative
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Submitted (MAY-2002)
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NUCLEOTIDE SEQUENCE.
STRAIN=129/SvcJ7;
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NUCLEOTIDE SEQUENCE.
STRAIN=129SvcJ7;
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SUCLECTIDE SEQUENCE.
SUCLECTIDE SEQUENCE.
STRAIN=129/SvcJ7, and 129SvcJ7;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
Obrile T., Huber C., van der Putten H., Schwab M.E.;
"Genomic structure and functional characterisation of the promoters of "Genomic structure""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ol-WAR-2003 (TrEMBLrel. 23, Created)
Ol-WAR-2003 (TrEMBLrel. 23, Last sequence update)
10-MAY-2003 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
RTM4 (Reticulon 4);
Mane=RLM4, ORRNames=RP23-17605.4-005;
Mus musculus (Mouse).
Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Muridae; Murinae; Muschontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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                                                                                                                                             A ray M., 1

Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.

R EMBL, AX102280; AAM73502.1; -; mRXA.

EMBL, AX102280; AAM73502.1; -; denomic_DNA.

R EMBL, AX1022814; AAM73502.1; -; Genomic_DNA.

R EMBL, AX1022814; AM73507.1; -; Genomic_DNA.

R EMBL, MJ91317; CAL24274.1; -; Genomic_DNA.

R EMBL, MG1.1915835; Rtn4.

R GO; GO:00020458; Mus musculus.

R GO; GO:0004305; C:cell projection; IDA.

R GO; GO:0005515; R:protein binding; IPI.

R GO; GO:0005515; R:protein binding; IPI.

R GO; GO:000599; R:pringenesis; IMP.

R GO; GO:000799; P:neurogenesis; IMP.

R GO; GO:000799; R:pringenesis; IDA.

R Pfan; PP02453; Reticulon.

R Pfan; PP02453; Reticulon; 1.

R PROSITE; PS06464; RETICULON; 1.

R PROSITE; PS06464; RETICULON; 1.
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
Putten H., Mir A.; de (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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100.0%; Pred. No. 1.6e-11;
ive 0; Mismatches 0;
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J. Mol. Biol. 325:299-323(2003).
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les 36; Conservative 0
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QBBGM9_MOUSE
ID QBBGM9_MOUSE PRELIMINARY;
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NUCLEOTIDE SEQUENCE.
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GrandPre T., Li S., Strittmatter S.M.;
"Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
Nature 417:547-551 (2002)
---- FUNCTION: Potent neutite outgrowth inhibitor which may also help
block the regeneration of the nervous central system in adults (By
                                                                                                                                                                                                                                                                                                                                                                                                                          -. SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the membrane of the endoplasmic reticulum through 2 putative transmembrane domains (By similarity).
-. Alfrenamive PRODUCTS:
-. Brent=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLECAIDE SEQUENCE (ISOFORMS 2 AND 4).

NUCLECAIDE SEQUENCE (TISSUE=Vascular smooth muscle;

STANIN-Wistar Kyoto; TISSUE=Vascular smooth muscle;

Ito T., Schwartz S.M.;

"Cloning of a member of the reticulon gene family in rat: one of two minor splice variants.";

Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mamalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUCLECTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
MEDLINE=20199258; PubMed=10667796; DOI=10.1038/35000219;
Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
Spillmann A.A., Christ F., Schwab M.E.;
"Nogo-A is a myellin-associated neurite outgrowth inhibitor and an
antigen for monoclonal antibody IN-1.";
Nature 403:434-439(2000).
                                                                                                                                                                                                                                                   RTN4 RAT

TO TANDARD; PRT; 1163 AA.

AC QUSKI1; QDROD9; QDWUE9; QDWUF0;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 47, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last sequence update)

DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)

DE Glutut vesicle 20 kDa protein).

GN Name=Rtn4; Synonymes-Nogo;

ON Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity)
SubsMrr: Binds to RTM4R. Interacts with Bcl-xl and Bcl-2 (By similarity)
                                                                                                                                                ;
                                                                                                      Local Similarity 100.0%; Score 175; DB 2; Length 1162; Les 36; Conservative 0; Mismatcher
GO; GO:0043025; C:cell soma; IDA.
GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0005215; F:procein binding; IPI.
GO; GO:0001525; P:angiogenesis; IMP.
GO; GO:0007329; P:neucogenesis; IDA.
InterPro; IPR003388; Reticulon.
Pfam; PR02453; Reticulon; 1.
BROSITE; PS50945; RETICULON; 1.
SEQUENCE 1162 AA; 126612 MM; 855697FBEE11781F CRC64;
                                                                                                                                                                                        1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
                                                                                                                                                                                                     1089
                                                                                                                               Query Match
                                                                                                                                                                                                                                          RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the as-

C uses as long as ...

DR EMBL, AJ242961; CAB71027.1; "RRNA.

BRELL, AJ242961; CAB71029.1; "RRNA.

DR EMBL, AJ242962; CAB71029.1; "RRNA.

DR EMBL, AJ242963; CAB71029.1; "RRNA.

DR EMBL, AJ242964; AAD31049.1; "RRNA.

DR EMBL, AD310406; AAD31049.1; "RRNA.

DR GO, GO: 0016021; C: integral to endoplasmic reticulum membrane; DR GO; GO: 0016021; C: integral to endoplasmic reticulum membrane; DR GO; GO: 0016021; C: integral to endoplasmic reticulum membrane; DR GO; GO: 0016021; P: protein binding; ISS.

DR GO; GO: 0016021; P: protein binding; ISS.

DR GO; GO: 0010517; P: negative regulation of axon extension; ISS.

DR GO; GO: 0010517; P: negative regulation of axon extension; ISS.

DR Fam, PPO2453; Reticulon; 1.

DR PROSITE; PSS0465; Reticulon; 1.

DR PROSITE; PSC0405; DR PROSITE; PSC0405; DR PROFENTIAL).

TOTO Lumenal (Potential).
                                                                                                                       Name=3; Synonyms=Nogo-C, VP20; Isold=09JK11-3; Squence-VSP_005656, VSP_005657; Name=4; Synonyms=Poocen-M2; Squence-VSP_005656, VSP_005657; Name=4; Synonyms=Poocen-M2; Squence-VSP_005659; Isold=09JK11-4; Squence-VSP_005659; TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are present in dorsal root ganglion, sciatic nerve and PC12 calls present in dorsal root ganglion, sciatic nerve and PC12 calls present in optic artilage, skin, lung and spleen. Isoforms 3 are detected in kidney, cartilage, skin, lung and spleen. Isoform 3 is expressed at high level in skeletal muscle. In adult animals isoform 1 is expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1130 1131 Missing (În Ref. 3; AAD31020).
1163 AA; 126388 MW; 8CB694B09E94F0B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lumenal (Potential).
Potential.
Cytoplasmic (Potential).
Reticulon.
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Missing (in isoform 2).
Frida-VSP 005656.
Missing (in isoform 2).
/Frida-VSP 005658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (in isoform 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1090 LKFAVLMWVFTYVGALFNGLTLILALISLFSIPVI 1125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTIG=VSP 005657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mainly in the nervous system.
Name=1; Synonyms=Nogo-A, NI-220-250;
ISOId=094XII-1; Sequence=1npplayed;
Name=2; Synonyms=Nogo-B, Foocen-M1;
IsoId=094XII-2; Sequence=VSP_005658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poly-Ala.
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TOPO DOM
TRANSMEM 9
TOPO DOM 10
TRANSMEM 111
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                       Query Match
Best Local Similarity 100.0%; Score 175; DB 2; Length 1245;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 36; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.4%; Score 174; DB 2; Length 187; 97.2%; Pred. No. 6.1e-12; Live 1; Mismatches 0; Indels
Wilson R.K.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
BMBL; AC013414; AAY24239.1; -; Genomic_DNA.
Hypothetical protein.
NON TER
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With any Propert B., Kang K.; -56013.";
Withe sequence of Homo sapiens BAC clone RP11-56013.";
Submitteed (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston R.H.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 187 AA; 20936 MW; A161F7A143C4607C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                13-88P-2005 (TrEMBLrel. 31, Created)
13-88P-2005 (TrEMBLrel. 31, Last sequence update)
13-8EP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothemical protein RTN4 (Fragment)
                                                                                                                                                                                                                            114 LKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 149
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                                                                                                                                                                                                    1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
                                                                                                                                                                                                                                                                                                                                                                     187 AA.
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Job time : 165.444 Becß
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Best Local Similarity 97.24
Matches 35, Conservative
                                                                                                                                                                                                                                                                                                                                               Q538Y1 HUMAN
ID Q538Y1_HUMAN PRELIMINARY;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=RTN4;
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OCASY1 HUMAN
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Koga H.;

Koga H.;

Koga H.;

The Complete Nucleotide Sequences of Mouse Homologues of KIAA Gene.

The Complete Nucleotide Sequences of Mouse KIAA-homologous CDNAs

Identified by Screening of Terminal sequences of CDNA Clones Randomly

Identified by Screening of Terminal sequences of CDNA Clones Randomly

Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.

RMGI, MGI.1915835, Rth4.

RMGI, MGI.1915835, Rth4.

RMGI, MGI.1915835, C:cell projection; IDA.

RGJ, GO:00042955, C:cell soma; IDA.

RGJ, GO:0005783; C:endoplasmic reticulum; IDA.

GO; GO:0005515; F:protein binding; IPI.

GO; GO:0001399; P:neurogenesis; IDA.

RICHEPRO; IPRO03398; Reticulon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
NAMIAA4153 protein (Fragment).
Name-Rtn4: Stronyms-mKIAA4153;
Mus musculus (Mouse).
Elkaryotcha; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
(NEBI TaxID=10090;
                                                                                                                                                                   Name=Rtn4;
Mus musculus (Mouse).
Bukaryotcu; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Muzinee; Mus.
NCBL_TAXID=L0090;
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Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Nagase T., Ohara O.,
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Best Local Similarity 100.0%; Score 175; DB 2; Length 1163;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 36; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                         01-007-2002 (TrEMBLrel. 22, Greated)
01-007-2002 (TrEMBLrel. 22, Last sequence update)
01-007-2003 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                             PRT; 1163 AA
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QSDTK9 MOUSE PRELIMINARY;
                             QBK3G8_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
        08K3G8 MOUSE
ALO 08K3G8-MC
DT 01-0CT-2g
DT 01-0CT-2g
DT 01-0CT-2g
DE Name-2A-6
GN Name-RAI-6
GN Mustaryote
CO Must
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Best Local Similarity 97.2%; Pred. No. 6.1e-15;
Matches 35; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           US-08-700-607-1

Sequence 1, Application US/08700607

Parent No. 5889708

Patent No. 5889708

APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.

TITLE OF INTERNION: THILIMAN, Jennifer L.

TITLE OF INTERNION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSER: Incyce Pharmaceuticals, Inc.

STREET: 9114 Porter Drive

CITY: Palo Alto
  US-09-134-000C 4234

US-09-252-991A-21088

US-09-252-991A-21625

US-09-134-000C-6126

US-09-134-000C-6126

US-09-134-000C-6126

US-09-138-425A-692

US-09-138-425A-692

US-09-134-000C-5431

US-09-134-000C-5431

US-09-134-000C-5431

US-09-134-000C-5431

US-09-134-000C-5431

US-09-107-522A-4817

US-09-107-522A-4817

US-09-107-522A-4817

US-09-177-486D-2

US-09-177-486D-2
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: SASTEM: DOS
SOFTWARE: FASTEM DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPRENCE/COCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 11: 415-855-055
INFORMATION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Ilmear
TOPOLOGY: Ilmear
TOPOLOGY: Ilmear
TOPOLOGY: Ilmear
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36,749
..... PF-0114 US
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consensus
         94304
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ZIP: 9430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
US-08-700-607-1
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Sequence 9124, Ap
Sequence 7, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6998, Ap
Sequence 4112, Ap
Sequence 4113, Ap
Sequence 8639, Ap
Sequence 873, Ap
Sequence 121, App
Sequence 121, App
Sequence 1251, App
Sequence 7290, Ap
Sequence 12517, App
Sequence 12517, App
Sequence 12517, Appli
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                                                                                                                                           February 17, 2006, 03:56:08; Search time 38.2222 Seconds (Without alignments) 77.869 Million cell updates/sec
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Sequence
Sequence
                               GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1. /cgn2 6/ptcdata1/iaa/5_COMB.pep:*

2. /cgn2 6/ptcdata1/liaa/6_COMB.pep:*

3. /cgn2 6/ptcdata1/liaa/H_COMB.pep:*

4. /cgn2 6/ptcdata1/liaa/PCTUS_COMB.pep:*

5: /cgn2 6/ptcdata1/liaa/RE_COMB.pep:*

6: /cgn2 6/ptcdata1/liaa/RE_COMB.pep:*
                                                                                                                                                                                                                      US-09-830-972A-2_COPY_1090_1125
175
1 LKPAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
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-09-949-016-7290
-09-489-039A-12517
-08-973-068-5
-09-540-236-2019
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-09-134-001C-4190
-09-248-796A-17364
-09-543-681A-4625
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US-08-700-607-8

US-08-700-607-8

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US-08-700-607-8

US-09-949-016-9180

US-09-149-016-6998

US-09-149-016-6998

US-09-149-016-6859

US-09-149-016-8859

US-09-149-016-8859

US-09-149-016-8859

US-09-149-016-8859

US-09-149-016-8859

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US-09-149-016-8859

US-09-149-016-8859

US-09-149-018-13008

US-09-148-018-13008

US-09-188-018-13008

US-09-188-018-13008
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                                                                                                                                                                                                                                                                                                                                                               572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                         BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                       Sequence:
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Gaps

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Query Match
Best Local Similarity 72.2%; Pred. No. 1e-11;
Matches 26; Conservative 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                              Query Match
85.7%; Score 150; DB 1; Length 208;
Best Local Similarity 72.2%; Pred. No. 7.9e-12;
Matches 26; Conservative 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-08-700-607-8
US-08-700-607-8
Sequence 8, Application US/08700607
Patent No. 5858708
APPLICANT: NYEORATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
MUMBERS OF SEQUENCES: 9
CORRESPER: 1374 POTER Drive
CITY: Palo Alto
STREET: 3174 POTER Drive
COMPUTER: 18M COMPALIBE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/700,607
APPLICATION NUMBER: US/08/700,607
APPLICATION NUMBER: Bild Herwith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
RESIRRENCE/DOCKET NUMBER: P1-014 US
TELEFAM: 415-465-655
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TTELEFAM: ATTORNESS: single
TELENCHE TRANDENCESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
LENGTH: 208 amino acids
; TYPE: amino acid
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ILBRARY: GenBank
; CLONE: 307311
US-08-700-607-7
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IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 281046
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US-08-700-607-8
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US-09-949-016-9124

Sequence 9124, Application US/09949016

Sequence 9124, Application US/09949016

Setent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: UNDER: US/09/949,016

CURRENT APPLICATION NUMBER: US/09/949,016

FRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

FRIOR PELING DATE: 2000-10-3

FRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRECED FOR WINDOWS VERSION 4.0

SEQ ID NO 9124

LENGTH: 201

TAVE: DETECTION PROPERTY OF THE PRIOR OF THE PRIOR 
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Sequence 7, Application US/08700607

Patent No. 5858708

APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Janice
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA.
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 LKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 163
                  126 LKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LKFAVLMWVFTYVGALFNGLTLLILLALISLFSIPVI 36
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ZIP: 94304.
ZIP: 94304.
ZIP: 94304.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION NOMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,749
RETERPHONE: 415-855-0555
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.2
Matches 35; Conservative
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CRGANISM: Human
US-09-949-016-9124
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                                                                                                                  Length 439;
                                                                                                                                                                                                                                                                                                                                  US-08-700-607-5

Sequence 5, Application US/08700607

Sequence 5, Application US/08700607

Sequence 5, Application US/08700607

Sequence 5, Application US/08700607

APPLICANT: Bandman, Olga

APPLICANT: Al-Young, Janice

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA
                                                                                                                    Query Match
85.7%; Score 150; DB 2; Length 435
Best Local Similarity 72.2%; Pred. No. 1.7e-11;
Matches 26; Conservative 9; Mismatches 1; Indels
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85.7%; Score 150; DB 1; Lo
Best Local Similarity 72.2%; Pred. No. 3.2e-11;
Matches 26; Conservative 9; Mismatches 1;
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                                                                                                                                                                                                                                 366 LKFAVLAMLLTYVGALFNGLTLLLAMAVVSMFTLPVV 401
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                                                                                                                                                                                                      1 LKFAVLMWVPTYVGALFNGLTLLILALISLFSIPVI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: CA
COUNTRY: U.S.
ZIP: 94304
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: EMA COMPATE:
OMBUTER: IBM COMPATE:
OMBUTER: DESCRIPTION DATA
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy U.
NAME: Billings, Lucy U.
RECESTRATION NUMBER: 36,749
RECESTRATION NUMBER: 36,749
RECESTRATION INFORMATION:
TELEPHONE: 415-844-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 776 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDENBES: single
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US-09-949-016-6998
'Sequence 6998, Application US/09949016
'Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLGCY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 307307
; SEQ ID NO 9180
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9180
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US-08-700-607-5
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i Sequence 9180, Application US/09949016

j Sequence 9180, Application US/09949016

j Patent No. 6812339

j GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WINBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

j FRIOR APPLICATION NUMBER: G0/241,755

pRIOR PELING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

pRIOR PILING DATE: 2000-09-03

pRIOR PILING DATE: 2000-09-03

pRIOR PILING DATE: 2000-09-03

j PRIOR PILING DATE: 2000-09-03

j PRIOR PILING DATE: 2000-09-03

j RANDER OF SEQ ID NOS: 207012

j SOFTWARE: FastSEQ for Windows Version 4.0
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85.7%; Score 150; DB 1; Length 356;
Best Local Similarity 72.2%; Pred. No. 1.4e-11;
Matches 26; Conservative 9; Mismatches 1; Indels
    STATE: CA.

STATE: CA.

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskettee

COMPUTER: IBM Compatible

SOFTWARE: FISH (SYSTA) NOWER: US/08/700,607

FILING DATE: FILed Herewith

ATTORNEY AGENT INCRAMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REGISTRATION NUMBER: PF-0114 US

TELEPOMONICATION INFORMATION:

TELEPOMONICATION INFORMATION:

TELEPOMONICATION INFORMATION:

TELEPOMONICATION OF SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 356 amino acide

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear TOPOLOGY: linear TYPE: peptide | IMMEDIATE SOURCE: LIBRARY: Genbank | CLONE: 307309 | US-08-700-607-6
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EARLIER APPLICATION NUMBER: 60/036,621
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-23
EARLIER FILING DATE: 19
            GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DIEBSE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL600107

CURRENT APPLICATION NUMBER: US/09/949.016

CURRENT PILING DATE: 2000-04-14

FRIOR PELLOR DATE: 2000-10-03

FRIOR PELLOR DATE: 2000-10-03

FRIOR PELLOR DATE: 2000-10-03

FRIOR PELLOR DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOGTWARER: FRIENCE FOR WINDOWS VERSION 4.0

SEQ ID NO 6998

LENGTH: 776

TENDER THE PELLOR DATE: 2000-09-09-08

SEQ ID NO 6998
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Sequence 45132, Application US/09270767
Sequence 45132, Application US/09270767
Sequence 45132, Application US/09270767
Sequence 45132, Application US/09270767
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
SOFWARE: PATENT: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SEQ ID NO 45132
LENGTH: 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 72.2%; Pred. No. 3.2e-11;
Matches 26; Conservative 9; Mismatches 1; Indels
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Patent No. 6420526
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
TITLE OF INVENTION: 186 Human Secreted proteins
PILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/99/149,476
CURRENT PILING DATE: 1998-09-08
BARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER APPLICATION NUMBER: 60/040,162
BARLIER APPLICATION NUMBER: 60/040,162
BARLIER APPLICATION WUMBER: 60/040,163
BARLIER APPLICATION WUMBER: 60/040,163
BARLIER APPLICATION WUMBER: 60/040,133
BARLIER PILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT CRGANISM: Drosophila melanogaster US-09-270-767-45132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Human
US-09-949-016-6998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-09-149-476-411
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EARLIER PILING DATE: 1997-04-11

BARLIER APPLICATION UNBER: 60/043,512

BARLIER PILING DATE: 1997-04-11

BARLIER PILING DATE: 1997-04-11

BARLIER PILING DATE: 1997-04-11

BARLIER PAPLICATION UNBER: 60/056,886

BARLIER PILING DATE: 1997-06-22

BARLIER PAPLICATION UNBER: 60/056,893

BARLIER PILING DATE: 1997-08-22

BARLIER PAPLICATION UNBER: 60/056,993

BARLIER PILING DATE: 1997-08-22

BARLIER PILING DATE: 1997-08-23

BARLIER PILING DATE: 199
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| MARLER APPLICATION NUMBER: 60/047614
| EMALIER PELINGUATION NUMBER: 60/043.576
| EMALIER PELINGUATION NUMBER: 60/043.576
| EMALIER PELINGUATION NUMBER: 60/043.576
| EMALIER PELINGUATION NUMBER: 60/045.670
| EMALIER PELINGUATION NUMBER: 60/045.670
| EMALIER PELINGUATION NUMBER: 60/056.632
| EMALIER PELINGUATION NUMBER: 60/056.632
| EMALIER PELINGUATION NUMBER: 60/056.631
| EMALIER PELINGUATION NUMBER: 60/051.631
| EMALIER PELINGUATION NUMBER: 60/050.631
| EMALIER PELINGUATION NUMBER: 60/040.632
| EMALIER PELINGUATION NUMBER: 60/040.632
| EMALIER PELINGUATION NUMBER: 60/040.632
| EMALIER PELINGUATION NUMBER: 60/040.633
| EMALIER PELINGUATION NUMBER: 60
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40,16; 47,60; 47,51; 47,50; 47,50; 47,58;	7047,617 7047,518 3047,503 3047,592 7047,592 7047,592 7047,500	3.3 3.047,632 3/043,580 11 1/043,580 1/043,314 1/1043,314 1/1043,569 1/1043,569 1/1043,673 1/1043,673 1/1043,673 1/1043,673 1/1043,673 1/1043,673 1/1043,313 1/1043,313 1/1043,673
2.03 - 0.	NUMBER: 60, 1997-05-25 (1997)	1997-05-2 1997-05-2 1997-05-2 1997-05-2 1997-04-1 NUMBER: 66 NUMBER: 66 1997-04-1 NUMBER: 66 NUMBER: 66 1997-04-1 NUMBER: 61
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EARLIER APPLICATION NUMBER: 60/056,886
EARLIER PILING DATE: 1997-08-26
EARLIER PILING DATE: 1997-08-26
EARLIER FILING DATE: 1997-08-26
EARLIER PRILING DATE: 1997-08-26
EARLIER PRILING DATE: 1997-08-27
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,812
EARLIER PRILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER PRILING DATE: 1997-08-23
EARLIER FILING DATE: 1997-08-23
EARLIER PRILING DATE: 1997-08-23
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EARLIER PRILING DATE: 1997-08-23
EARLIER PRILING DATE: 1997-08-23
EARLIER PRILING DATE: 1997-08-23
EARLIER FILING DATE: 1997-08-23
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Sequence 7220, Application US/09949016

Sequence 7220, Application US/09949016

Set 10. Reliable

APPLICANT: USRYER, J. Craig et al.

APPLICANT: USRYER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR PILING DATE: 2000-10-03
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                                                                                                                                                                                   Sequence 3, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bar-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 LKCLAVFWWLMTYVGAVFNGITLLILAELLIFSVPIV 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: U.S. ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: Fast SEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0114 US
TELEGOMMUNICATION INFORMATION:
TELEGOMMUNICATION INFORMATION:
TELEGOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ 1D NO: 3.
SEQUENCE CHARACTERISTICS:
LENGTH: 241 Ami-
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amino acid
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IMMEDIATE SOURCE:
LIBRARY: THPINOB01
CLONE: 31870
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TOPOLOGY: linear
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US-09-949-016-7290
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US-09-949-016-8859

is Sequence 8859, Application US/09949016

j Sequence 8859, Application US/09949016

j Retent No. 6812339

j GENERAL INFORMATION:

TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TILLE OF INVENTION: WITH HUMAN DISEABS, METHODS OF DETECTION AND USES THEREOF

TILLE OF INVENTION: WITH HUMAN DISEABS, METHODS OF DETECTION AND USES THEREOF

TILLE OF INVENTION: WITH HUMAN DISEABS, METHODS OF DETECTION AND USES THEREOF

TILLE OF INVENTION: WITH HUMAN DISEABS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT PELLING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFWWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8859

LENGTH: 192
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74.9%; Score 131; DB 2; Length 192;
Best Local Similarity 63.9%; Pred. No. 2e-09;
Matches 23; Conservative 8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
74.9%; Score 131; DB 2; Length 16
Best Local Similarity 63.9%; Pred. No. 1.7e-09;
Matches 23; Conservative 8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 60/043,670
EARLIER PLILAGA DATE: 1997-04-13
EARLIER PLILAGA DATE: 1997-04-13
EARLIER PLILAGA DATE: 1997-04-13
EARLIER PLING DATE: 1997-08-22
EARLIER PLING DATE: 1997-08-26
EARLIER PLING DATE: 1997-08-26
EARLIER PLING DATE: 1997-09-05
                  DATE: 1997-05-23
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| PRIOR RPPLICATION NUMBER: 60/211,498
| PRIOR PREDICATION NUMBER: 60/211,498
| PRIOR PREDICATION NUMBER: 0207012
| SOFTWARE: PEEESBO FOR WINDOWN Vereion 4.0
| SECOND IN 07.000 | PRIOR PREDICATION NUMBER: PEEESBO FOR WINDOWN VEREIN 1.00 | PRIOR PREDICATION NUMBER: 020 | PRIOR PRIOR PREDICATION NUMBER: 020 | PRIOR PRI
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Sequence 6, Appliseduence 6, Appliseduence 71, Appliseduence 72, Appliseduence 429, Appliseduence 9, Appliseduence 9, Appliseduence 9, Appliseduence 3, Appliseduence 3, Appliseduence 3, Appliseduence 7, Appliseduence 17, Appliseduence 17, Appliseduence 17, Appliseduence 17, Appliseduence 17, Appliseduence 17, Appliseduence 6, A

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US-09-789-386-2
US-09-789-140-6
US-09-893-348-2
US-09-993-348-2
US-10-660-05-71
US-10-660-05-71
US-10-660-13-9
US-10-466-28-9
US-10-466-391A-9
US-10-466-391A-9
US-110-090-836-3
US-110-090-836-3
US-110-090-836-3
US-110-660-946-7
US-110-660-946-7
US-110-660-946-7
US-110-660-946-7
US-110-660-946-7
US-110-660-946-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/09893348 Patent No. US20020072493A1 GENERAL INFORMATION:
         11192
11192
11192
11192
11192
11192
11192
11192
208
208
208
356
         -09-893-348-21
             21, Appl
20, Appl
20, Appl
16, Appl
10, Appl
10, Appl
10, Appl
11, Appl
25, Appl
11, Appl
25, Appl
11, Appl
11,
                                                                                                                                                                                                        February 17, 2006, 03:57:08; Search time 130.222 Seconds (without alignmente) (without alignmente) 115.509 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA_Main:*
1: /cgn2 6/ptodate/l/pubpaa/USOT_PUBCOMB.pep:*
2: /cgn2 6/ptodate/l/pubpaa/USO9_PUBCOMB.pep:*
3: /cgn2 6/ptodata/l/pubpaa/USO9_PUBCOMB.pep:*
4: /cgn2 6/ptodata/l/pubpaa/USIOA_PUBCOMB.pep:*
5: /cgn2 6/ptodata/l/pubpaa/USIOB_PUBCOMB.pep:*
6: /cgn2 6/ptodata/l/pubpaa/USIOB_PUBCOMB.pep:*
                                          GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                     US-09-830-972A-2_COPY_1090_1125
175
1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
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US-09-893-348-21

US-10-810-653-20

US-10-810-653-20

US-10-205-194-164

US-10-205-194-164

US-10-205-194-110

US-10-207-502-431

US-10-810-653-18

US-10-810-653-18

US-10-998-33-48-18

US-10-998-33-48-18

US-10-998-33-615

US-10-10-653-184

US-10-10-653-186

US-10-10-653-186

US-10-10-653-186

US-10-10-653-186

US-10-10-653-186

US-10-10-660-066

US-10-10-060-066-12

US-10-060-066-12

US-10-060-066-12

US-10-060-066-12

US-10-060-066-12

US-10-060-066-12

US-10-060-066-12

US-10-066-136-14

US-10-066-136-14

US-10-066-136-14

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US-10-066-136-14
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
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                                                                                                                                                                                                                      Run on:
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GENERAL INCRANTION HERE

APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: COHEN, ITUN R.

APPLICANT: MOSONEGO, Alon
APPLICANTON NUMBER: US/09/893,348
CURRENT APPLICATION NUMBER: US/09/893,348
CURRENT APPLICATION NUMBER: US/09/314,161
PRIOR FILING DATE: 1999-05-19
PRIOR PLING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: PCT/US/08/14715
PRIOR APPLICATION NUMBER: IL 124500
PRIOR APPLICATION NUMBER: IL 124500
PRIOR FILING DATE: 1998-05-19
PRIOR PLING DATE: 1998-05-19
SOFTWARE: PATENTIN VERSION 3.1
SOFTWARE: PATENTIN VERSION 3.1
FENDRE PATENTIN PATE: 1998-05-19
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-10-810-653-21
US-10-810-653-21
APDICATION NO. US20040253218A1
Sequence 21, Application US/10810653
PUBLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: BISERNAN, Pierre
APPLICANT: MOSONSCO, Alon
APPLICANT: MOSONSCO, Alon
APPLICANT: MOSURSCO, ALON
ATTLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 175; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.6e-14;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-893-348-21
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Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence

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APPLICANT: EISENBACH.
APPLICANT: EISENBACH.
APPLICANT: EISENBACH.
APPLICANT: COHEN, ITUM R.
APPLICANT: MOSONEGO, ALON
APPLICANT: MONERER: US/10/891,653
CURRENT APPLICATION NUMBER: US/09/893,348
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR PALLOATION NUMBER: US 09/218,277
PRIOR FILING DATE: 1999-07-21
PRIOR PLILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: IL 124500
PRIOR APPLICATION NUMBER: IL 124500
PRIOR PLILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 20
MANDER: PARENTIN ON SEQ ID NOS: 29
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US-10-205-194-164
US-10-205-194
US-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 100.0%; Score 175; DB 5; Length 360; Local Similarity 100.0%; Pred. No. 3e-14; neg 36; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT; ORGANISM: Rattus norvegicus
US-10-810-653-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: COHEN, Irun R.
APPLICANT: COHEN, Irun R.
APPLICANT: COHEN, Irun R.
APPLICANT: MOALEM, Gila
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
FILE REPRENCE: EIS-SCHWARTZ-2A
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
FILE REPRENCE: EIS-SCHWARTZ-2A
FRIOR REPLICATION WUMBER: US 09/314,161
PRIOR PELICATION NUMBER: US 09/314,161
PRIOR PELICATION NUMBER: US 09/218,277
PRIOR PELICATION NUMBER: US 09/218,277
PRIOR PELICATION NUMBER: PCT/US98/14715
PRIOR PELICATION NUMBER: PCT/US98/14715
PRIOR APPLICATION NUMBER: PCT/US98/14715
PRIOR PELICATION NUMBER: 1998-07-21
PRIOR PELICATION NUMBER: 1998-07-21
PRIOR PELICATION NUMBER: 11,124500
PRIOR PELICATION NUMBER: 1998-05-19
NUMBER OF SEQ ID NOS: 29
LENGTHRE: PARENCE PAR
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100.0%; Score 175; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 3e-14;
Matches 36; Conservative 0; Mismatches 0; Indels
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100.0%; Score 175; DB 5; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.6e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0
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                                                   PILE REFERENCE: EIS-SCHWARTZ=2A
(CURRENT PELLING NUMBER: US/10/810,653
CURRENT FILING DATE: 2004-03-29
PRIOR APPLICATION NUMBER: US/09/893,348
PRIOR PILING DATE: 2001-06-28
PRIOR PLING DATE: 1999-05-19
PRIOR PLING DATE: 1999-05-19
PRIOR PLING DATE: 1999-05-19
PRIOR PLING DATE: 1998-07-17
PRIOR PLING DATE: 1998-07-17
PRIOR PLING DATE: 1998-07-17
PRIOR FILING DATE: 1998-07-18
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US-10-653-20
Sequence 20, Application US/10810653
Sequence 20, O. US20040253218A1
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ORGANISM: Rattus norvegicus
US-09-893-348-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 199
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-810-653-21
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MCS-10-010-653-18

Sequence 18, Application US/10810653

Sequence 18, Application US/2024023218A1

Publication No. US20040253218A1

REPRICANT: EISENBARCH-SCHWARTZ, Michal

APPLICANT: COHEN, Irun R.

APPLICANT: MOSONEGO, Alon

APPLICANT: MOSONEGO, Alon

APPLICANT: MOLEM, Gila

APPLICANT: WOLEM, Gila

CURRENT PERING DATE: 2004-03-29

PRIOR APPLICATION NUMBER: US/09/993,348

PRIOR APPLICATION NUMBER: US/09/993,348

PRIOR PELING DATE: 1999-05-19

PRIOR FILING DATE: 1999-05-19
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100.0%; Score 175; DB 4; Length 1163;
Best Local Similarity 100.0%; Pred. No. 9.7e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 431, Application US/10267502
Sequence 431, Application US/10267502
Publication No. US20040071700A1
GENERAL INFORMATION:
APPLICANT: Kim, Jaescob
APPLICANT: Galant, Ron
TITLE OF INVENTION: Obesity Linked Genes
FILE REFERENCE: LSD-07416
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SOFTAME: PatentIn version 3.2
SEQ ID NO 431
INFORT. 1163
CURRENT APPLICATION NUMBER: US/09/893,348
CURRENT FILING DATE: 2001-06-28
PRIOR PELING DATE: 1999-06-19
PRIOR PILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: US 09/218,277
PRIOR APPLICATION NUMBER: PCT US98/14715
PRIOR PILING DATE: 1998-07-21
PRIOR PILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-07-31
SOFTWARE: PARENTIN NUMBER: IL 12450
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PARENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
COGANISM: Rattus norvegicus
US-09-893-348-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Mus musculus
US-10-267-502-431
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Batent No. US20020072493A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: EISENBACH-SCHWARTZ, Michal

APPLICANT: COHEN, Irun R.

APPLICANT: HOSONEGO, Alon

APPLICANT: MOSONEGO, Alon

APPLICANT: MOSONEGO, Alon

TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE

PILE REFERENCE: EIS-SCHWARTZ=2A
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15-427-
                  US-10-633-423-10

JS-SQUARDER 10.0 Application US/10633423

PUBLICARION NO. US20040121240A1

GENERAL INPORMATION:

APPLICANT: Tobyama, Masaya

APPLICANT: Tobyama, Masaya

APPLICANT: Tobyama, Masaya

TILE OF INVENTION NOWER: 10510-0323. USO

CURRENT PELLING NAMES: 10510-0323. USO

CURRENT FILING DATE: 2003-07-11

PRIOR APPLICATION NUMBER: US/10/633,423

CURRENT FILING DATE: 2003-07-11

PRIOR APPLICATION NUMBER: JP 2003-92923

PRIOR APPLICATION NUMBER: JP 2003-92923

PRIOR PILING DATE: 2003-03-12

SOFTWARE: PATENTING DATE: 2003-03-12

SOFTWARE: PATENT NUMBER: JP 2003-92923

NUMBER OF SEQ ID NOS: 27.1

SOFTWARE: PATENT NUMBER: JP 2003-92923

TYPE: PRT

CREATION NUMBER OF SEQ ID NOS: 27.1

SOFTWARE: PATENT NUMBER: JP 2003-92923

TYPE: PRT

CREATION NUMBER OF SEQ ID NOS: 27.1

SOFTWARE: PATENT NUMBER: JP 2003-92923

TYPE: PRT

CREATION NUMBER OF SEQ ID NOS: 27.1

SOFTWARE: PATENT NUMBER: JP 2003-92923

TYPE: PRT

CREATION NUMBER OF SEQ ID NOS: 27.1

SOFTWARE: PATENT NUMBER: JP 2003-92923

TYPE: PRT

CREATION NUMBER OF SEQ ID NOS: 27.1

SOFTWARE: PATENT NUMBER: JP 2003-92923
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100.0%; Score 175; DB 4; Length 1162;
Best Local Similarity 100.0%; Pred. No. 9.7e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 9.7e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1089 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 1124
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CRGANISM: Mus musculus
US-10-427-741-10
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TITLE OF INVENTION: 66 Human Secreted Proteins
FILE REFERENCE: P2008PLC2
CURRENT FILING DATE: 2005-04-22
CURRENT PILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US/11/111, 953
RIOR PILING DATE: 1996-13
PRIOR PILING DATE: 1996-13
PRIOR PILING DATE: 1996-12-11
PRIOR PAPLICATION NUMBER: 0/209,462
PRIOR PAPLICATION NUMBER: 0/209,462
PRIOR PAPLICATION NUMBER: 0/049,547
PRIOR PAPLICATION NUMBER: 60/049,547
PRIOR PLING DATE: 1997-06-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1090 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 1125
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; LOCATION: (175)
; OTHER INPORMATION: Xaa equals stop translation
US-11-111-93-184
PRIOR APPLICATION NUMBER: US 09/218,277
PRIOR PLING DATE: 1998-12-22
PRIOR PLING DATE: 1998-12-22
PRIOR PLING DATE: 1998-07-21
PRIOR PLING DATE: 1998-07-21
PRIOR PLING DATE: 1998-05-19
PRIOR PLING DATE: 1998-05-19
SPURE PLING DATE: 1998-05-19
SPURE: PAREIN PRIOR PLING DATE: 1998-05-19
SEQ ID NO 18
LENGTH: 1163
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US-11-11-953-184
US-11-11-953-184

Sequence 184, Application US/11111953

Publication No. US20050214844A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Rattus norvegicus US-10-810-653-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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Seguence 25, 248-25

SEGUENCE 25, 2801cation US (19893148)

FREETEN W. USEROZONOZ493141

FREETEN W. USEROZONOZ 14144121

FREETEN W. USEROZONOZ MURGER: US 09/124,277

FREEZEN W. USEROZONOZ MURGER: US 09/124,277
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Gaps

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RESULT 15
US-104-08-967-9
US-104-08-967-9
Sequence 9, Application US/10408967
Sequence 9 Application No. US20040063161A1
GENERAL INFORMATION:
APPLICANT: Pan, Ridiang
APPLICANT: Tan, Ridiang
TITLE REPERENCE: 00925
TITLE REPERENCE: 00925
CURRENT FILING DATE: 2003-04-08
CURRENT FILING DATE: 2003-04-08
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
99.4%; Score 174; DB 4; Length 199;
Best Local Similarity 97.2%; Pred. No. 2.2e-14;
Matches 35; Conservative 1; Mismatches 0; Indels
                 Query Match

99.4%; Score 174; DB 4; Length 199;
Best Local Similarity 97.2%; Pred. No. 2.2e-14;
Matches 35; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 LKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 161
                                                                                                                                                                               126 LKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: February 17, 2006, 04:03:21 Job time : 131.222 BecB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-967-9
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PRIOR APPLICATION NUMBER: US 09/247,155
PRIOR FILING DATE: 1999-02-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 810
SEQ ID NO 467
LENGTH: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-660-946-1

| Sequence 1, Application US/10660946
| Publication No. US20040063131A1
| Publication No. US20040063131A1
| Publication No. US20040063131A1
| Publication No. US20040063131A1
| Au-Young, Janice Goli, Surya A. Young, Janice Goli, Surya A. Young, Janice Hillman, Jennifer L. |
| TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS NUMBER OF SEQUENCES: 9
| CORRESPONDENCE ADDRESS: 9
| CORRESPONDENCE ADDRESS: 9
| CORRESPONDENCE ADDRESS: 9
| CORRESPONDENCE ADDRESS: 9
| CORPUTER: Palo Alto STREET: 13/4 Porter Drive CITY: Palo Alto COMPUTER: BALOALDE FORM: MEDITE: Palo Alto OFFILM TYPE: Diskette OFFILM TYPE: DISKET NUMBER: 35,749
| RESPERANCE/DOCKET NUMBER: 36,749
| RELECOMMUTCATION INDERNATION: NAME: BILLINGS: LUCY J. REPRENCE AID NO: TEMPORE 
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
99.4%; Score 174; DB 3; Length 19:
Best Local Similarity 97.2%; Pred. No. 2.2e-14;
Matches 35; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 LKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 161
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                 ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -42..-1
US-09-978-360A-467
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US-10-660-946-1
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RESULT 2
US-11-044-899-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                        February 17, 2006, 03:58:38; Search time 11.5556 Seconds (without alignments) 44.284 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_AA_New:*

1: /cgn2_6/ptodata/l/pubpaa/US08_NEW_PUB.pep:*

3: /cgn2_6/ptodata/l/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/l/pubpaa/US07_NEW_PUB.pep:*

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6: /cgn2_6/ptodata/l/pubpaa/NEW_PUB.pep:*

7: /cgn2_6/ptodata/l/pubpaa/NEW_PUB.pep:*

8: /cgn2_6/ptodata/l/pubpaa/US10_NEW_PUB.pep:*

9: /cgn2_6/ptodata/l/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                              US-09-830-972A-2_COPY_1090_1125
175
1 LKPAVLMWVFTYVGALFNGLTLLILALISLFSIFVI 36
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US-11-044-899-2
US-11-044-899-30
US-11-044-899-34
US-09-978-160A-467
US-10-821-234-1170
US-11-044-899-23
US-11-044-899-23
US-11-044-899-22
US-11-044-899-27
US-11-044-899-27
US-11-044-899-27
US-11-044-899-27
US-11-044-899-27
US-11-044-899-27
US-11-045-897-111
US-10-055-877-111
US-10-055-877-115
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US-11-229-371-123
US-11-228-923-123
                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                107819 seqs, 14214640 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
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Sequence 2, Application US/11044899
Publication No. US20050260616A1
GENERAL INFORMATION:
GENERAL THORDANATION:
APPLICANT: Schwab, M.
APPLICANT: Chen, M.
TITLE OF INVENTION: WILEDOIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED TITLE OF INVENTION: THEREON
FILE REFERENCE: 10200-017-999
CURRENT PELLION NUMBER: US/11/044,899
CURRENT FILING DATE: 2005-01-26
PRIOR APPLICATION NUMBER: 09/830,972
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Sequence 113, App
Sequence 305, App
Sequence 307, App
Sequence 180, App
Sequence 180, App
Sequence 460, App
Sequence 256, App
Sequence 1842, Ap
Sequence 11842, Ap
Sequence 116, App
Sequence 316, App
Sequence 316, App
Sequence 57, Appl
Sequence 57, Appl
Sequence 59, Appl
Sequence 59, Appl
Sequence 2584, App
Sequence 2584, App
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 36; Conservative 0; Mismatches 0;
 US-11-229-371-113

US-10-055-877-306

US-10-055-877-307

US-11-044-3478-2

US-11-044-3478-2

US-11-044-3478-2

US-11-044-3478-2

US-11-044-3478-2

US-10-93-626-4460

US-10-93-626-2564

US-10-093-626-1442

US-11-086-686-10850

US-11-086-686-10850

US-11-086-412-58

US-11-166-412-58

US-11-166-412-59

US-11-166-412-59
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                                                                                                                                                                                                                ALIGNMENTS
              199119999199111
    RESULT 1
US-11-044-899-25
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RESULT 5
RESULT 5
RESULT 5
Sequence 467, Application US/09978360A
Sequence 467, Application US/09978360A
Sequence 467, Application No. US2006009633A9
SEQUENCE 467, Application No. US2006009633A9
SEQUENCE 47, Application No. US200600963A9
SEPLICANT: DAGGET, Aymeratic Education
APPLICANT: DAGGET, Aymeratic Education
APPLICANT: DOGGET Several
APPLICANT: Object Several
APPLICANT: Object Several
APPLICANT: Object Several
APPLICANT: Object Several
APPLICANT: US/09/978,360A
CURRENT APPLICATION NUMBER: US/09/978,360A
CURRENT APPLICATION NUMBER: US/0606,677
PRIOR RELING DATE: 1997-11-13
PRIOR PLING DATE: 1999-12-17
PRIOR PLING
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99.4%; Score 174; DB 5; Length 199;
Best Local Similarity 97.2%; Pred. No. 2.5e-15;
Matches 35; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Query Match

99.4%; Score 174; DB 7; Length 186;
Best Local Similarity 97.2%; Pred. No. 2.3e-15;
Matches 35; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/830,972
PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: PCT/US99/26160
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-06
NUMBER OF SEQ ID NOS: 51
SOFWARE: FREUSEQ for Windows Version 3.0
LENGTH: 186
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: SIGNAL
; LOCATION: -42...1
US-09-978-360A-467
                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: BOS SP.
US-11-044-899-24
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US-11-044-899-24
US-11-044-899-24
Sequence 24, Application US/11044899
Sequence 24, Application WS/11044899
Publication No. US20050260616A1
GENERAL INFORMATION:
APPLICANT: Chem. M.
APPLICANT: Chem. M.
APPLICANT: Chem. M.
TITLE OF INVENTION: THEREON
TITLE OF INVENTION: THEREON
FILE REPRESENCE: 10200-017-999
CURRENT APPLICATION NUMBER: US/11/044,899
CURRENT FILING DATE: 2005-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PREDICANT: Growth.

APPLICANT: Growth.

TITLE OF INVENTION: NUCLECTIDE AND PROTEIN SEQUENCES OF NOCO GENES AND METHODS BASED
TITLE OF INVENTION: THEREON
TITLE OF INVENTION: THEREON
TITLE OF INVENTION: THEREON
TITLE OF INVENTION: THEREON
TITLE OF INVENTION TOWER: US/11/044,899
CURRENT PAPLICATION NUMBER: US/11/044,899
CURRENT APPLICATION NUMBER: 09/126
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 1999-11-05
PRIOR PLILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
SOFTWARE: Fast ID NOS: 51
SOFTWARE: Fast ID NOS: 51
SOFTWARE: Fast ID NOS: 51
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Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0;
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                ; FEATURE:
NAMEKEY: VARIANT
LOCATION: (1)...(1163) at all Xaa position
COTHER INFORMATION: Xaa = any amino acid
US-11-044-899-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-11-044-899-30
Sequence 30, Application US/11044899
Publication No. US20050260616A1
GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
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RESULT 8

US-11-044-899-23

US-11-044-899-23

Sequence 23, Application US/11044899

Publication No. US2005026061641

Sequence 23, Application US/11044899

Publication No. US2005026061641

APPLICANT: Schwab, M.

APPLICANT: Schwab, M.

TITLE OF INVENTION: THEREON

PRIOR FILING DATE: 2001-09-24

PRIOR FILING DATE: 2001-09-24

PRIOR FILING DATE: 1999-11-06

PRIOR FILING DATE: 1999-11-06

PRIOR FILING DATE: 1999-11-06

NUMBER OF SEQ ID NOS: 51

SEQ ID NOS: 51

SEQ ID NO 23

LENGTH: 186

LENGTH: 186
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1 Sequence 21, Application US/11044899

5 Sequence 21, Application US/11044899

5 Publication No. US20050260616A1

GENERAL INFORMATION:

APPLICANT: Schwab, M.

APPLICANT: Chen, M.

TITLE OF INVERTION: THEREON

TITLE OF INVERTION: THEREON

TITLE OF INVERTION: THEREON

FILE REFRENCE: 10200-017-999

CURRENT APPLICATION NUMBER: 00/810,972

PRIOR PILING DATE: 2001-09-24

PRIOR PLILNG DATE: 1999-11-05

PRIOR APPLICATION NUMBER: 60/107,446

PRIOR PLILNG DATE: 1999-11-05

PRIOR APPLICATION NUMBER: 60/107,446

PRIOR PLILNG DATE: 1999-11-06

SEQ ID NOS: 51

SOFTWARE: FEAL SEQ for Windows Version 3.0

LENGTH: 186
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85.7%; Score 150; DB 7; Length 186
Best Local Similarity 72.2%; Pred. No. 2.4e-12;
Matches 26; Conservative 9; Mismatches 1; Indels
1105 LKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 1140
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86.9%; Score 152; DB 7;
Best Local Similarity 75.0%; Pred. No. 1.4e-12;
Matches 27; Conservative 8; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT; Gallus gallus US-11-044-899-23
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US-11-044-899-21
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105-11-044-899-29

15 Gequence 29, Application US/11044899

16 Gequence 29, Application US/11044899

17 Explication Wo. US20050260616A1

18 CENTRAL INFORMATION: Chen, M.

18 PILLE OF INVENTION: WICLECTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED

18 TITLE OF INVENTION: WICHEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED

18 TITLE OF INVENTION: THEREOFY

18 TITLE OF INVENTION: WHERE: 2005-01-26

19 CURRENT APPLICATION NUMBER: 09/830,72

19 PRIOR APPLICATION NUMBER: 09/830,72

19 PRIOR FILING DATE: 1099-11-05

10 PRIOR APPLICATION NUMBER: PCT/US99/26160

10 PRIOR APPLICATION NUMBER: PCT/US99/26160

10 PRIOR FILING DATE: 1999-11-05

10 PRIOR FILING DATE: 1999-11-06

10 NUMBER: PCT OF ONE SEQ ID NOS: 51

11 PARTICATION NUMBER: PCT OF ONE SEQ ID NOS: 51

10 PRIOR FILING DATE: 1099-11-06

10 PRIOR FILING DATE: PUMPER: PCT OF ONE SEQ ID NOS: 51

11 PARTICATION NUMBER: PCT OF ONE SEQ ID NOS: 51

11 PARTICATION DATE: PCT OF ONE SEQ ID NOS: 51

11 PARTICATION DATE: PCT OF ONE SEQ ID NOS: 51

11 PARTICATION DATE: PCT OF ONE SEQ ID NOS: 51

11 PARTICATION DATE: PCT OF ONE SEQ ID NOS: 51

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11 PARTICATION DATE: PCT OF ONE SEQ ID NOS: 51

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11 PARTICATION DATE: PCT OF ONE SEQ ID NOS: 51
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                                                                                                                                           RESULT 6
US-10-821-34-1170
US-10-821-34-1170

| Sequence 1170, Application US/10821234
| Sequence 1170, Application No. US20050255114A1
| GENERAL INFORMATION:
| APPLICANT: Labat, IVan
| APPLICANT: Stache-Crain, Birgit
| APPLICANT: Aradamani, Susan
| APPLICANT: Aradamani, Tom
| APPLICANT: Tang, Y. Tom
| APPLICANT: Tang, Y. Tom
| APPLICANT: Tang, Y. Tom
| GURRENT APPLICATION: Methods for Diagnosis and Treatment of Preeclampsia
| CURRENT APPLICATION NUMBER: US/10/821,234
| CURRENT APPLICATION NUMBER: US/04-04-07
| PRIOR PILING DATE: 2003-04-07
| RIONARE OF SEQ ID NOS: 1704
| SOFTWARE: DE SEQ_Genes Version 1.0
| SEQ ID NOS: 1704
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99.4%; Score 174; DB 7; Length 11'
Best Local Similarity 97.2%; Pred. No. 1.4e-14;
Matches 35; Conservative 1; Mismatches 0; Indels
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LOCATION: (1)...(1178) at all Xaa position

CATHER INFORMATION: Xaa = any amino acid
US-11-044-899-29
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TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-821-234-1170
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Best Local 9
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GENERAL INCORPATION:

APPLICANT: Schwab, M.

APPLICANT: Schwab, M.

TITLE OF INVENTION: THEREOW

CURRENT APPLICATION UNMERS: 09/830,972

PRIOR APPLICATION WHORER: 201-09-24

PRIOR APPLICATION WHORER: POT/US99/26160

PRIOR PELLOR DATE: 2010-09-24

PRIOR PELLOR DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-06

NUMBER OF SEQ ID NOS: 51

SOFTWARE PERSON OF SEQ ID NOS: 51

SOFTWARE PERSON OF STATE OF SEQ ID NOS: 51

SEQ ID NO 27
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US-10-505-263-83
US-10-505-263-83

Sequence 83, Application US/10505263

Sequence 83, Application Wo. USC0060014940A1

GENERAL INFORMATION:
APPLICANT: Vanderbilt University
APPLICANT: The Brigham and Women's Hospital, Inc.
APPLICANT: Mount. David B
APPLICANT: Mount. David B
APPLICANT: Mount. David B
APPLICANT: Romero, Michael
ITIE OF INVENTION: CLOMING AND CHARACTERIZATION OF SLC26A6, SLC26A1, and SLC26A2

TILE REPERBENCE: 1242/50/2 PCT/US
CURRENT PILING DATE: 2004-08-20

PRIOR FILING DATE: 2004-08-20

PRIOR FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-28

SPRIOR FILING DATE: 2003-02-28

SUFFMARE: Patentin version 3.2

SEQ ID NO 83

LENTH: 769

LENTH: 769

LENTH: 769
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460    RWDAVIWVFTCVSAIILGLDLGLLA 484
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US-10-505-263-81
i, Sequence 81, Application US/10505263
; Publication No. US20060014940A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
; ORGANISM: D. melanogaster
US-11-044-899-27
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CORGANISM: Xenopus laevis
US-10-505-263-83
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105-11-044-899-26
1 Sequence 26. Application US/11044899
1 Publication No. US20050260616A1
2 GENERAL INVORVATION:
1 APPLICANT: Schwab, M.
2 APPLICANT: CAPE, M.
2 TITLE OF INVENTION: THEREON
2 TITLE OF INVENTION: THEREON
3 FILE REFREENCE: 10200-017-99
3 CURRENT PLIANG DATE: 2005-017-96
4 PRIOR PILING DATE: 2005-01-06
5 PRIOR APPLICATION NUMBER: US/11/044,899
5 CURRENT PLIANG DATE: 2009-024
6 PRIOR FILING DATE: 1999-11-05
7 PRIOR FILING DATE: 1999-11-05
8 PRIOR FILING DATE: 1999-11-06
8 NUMBER OF SEQ ID NOS: 51
8 SOFTWARE: RESURE OF Windows Version 3.0
8 SEG ID NO 26
8 LEMOTH: 194
                                              Sequence 22, Application US/11044899

Sequence 22, Application US/11044899

Publication No. US205026616A1

GENERAL INFORMATION:

APPLICANT: Schwab, M.

APPLICANT: Schwab, M.

TITLE OF INVENTION: THEREON

TITLE OF INVENTION: THEREON

TITLE OF INVENTION: THEREON

TITLE OF INVENTION: THEREON

PRIOR APPLICATION NUMBER: US/11/044,899

CURRENT APLICATION NUMBER: US/12

PRIOR APPLICATION NUMBER: 60/107,46

PRIOR PLING DATE: 1999-11-05

PRIOR PLING DATE: 1999-11-06

PRIOR FILING DATE: 1999-11-06

PRIOR FILING DATE: 1999-11-06

NUMBER OF SEQ ID NOS: 51

LENGWARE: PESTERE SET SEG FOR Windows Version 3.0

SSO ID NO 22

LENGUTH: 186
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55.4%; Score 97; DB 7; Length 194;
Best Local Similarity 41.7%; Pred. No. 1.2e-05;
Matches 15; Conservative 11; Mismatches 10; Indels
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85.7%; Score 150; DB 7;
Best Local Similarity 72.2%; Pred. No. 2.4e-12;
Matches 26; Conservative 9; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-11-044-899-27
Sequence 27, Application US/11044899
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CRGANISM: C. elegans
US-11-044-899-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Rattus sp.
US-11-044-899-22
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PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-03-30
PRIOR PILING DATE: 2001-03-30
PRIOR PILING DATE: 2001-03-30
PRIOR PILING DATE: 2001-03-14
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28.6%; Score 50; DB 6; Length 252;
Best Local Similarity 30.8%; Pred. No. 13;
Matches 8; Conservative 8; Mismatches 10; Indels
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CORGANISM: Homo sapiens
US-10-055-877-107
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                            APPLICANT: Vanderbilt University
APPLICANT: Vanderbilt University
APPLICANT: Case Western Reserve University
APPLICANT: The Brigham and Women's Hospital, Inc.
APPLICANT: Mount, David B
APPLICANT: ROMEOO, Michael
ITLE OF INVENTION: CLONING AND CHARACTERIZATION OF SLC26A6, SLC26A1, and SLC26A2
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF SLC26A6, SLC26A1, and SLC26A2
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF SLC26A6, SLC26A1, and SLC26A2
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF SLC26A6, SLC26A1, and SLC26A2
CURRENT APPLICATION NUMBER: US 60/360,275
PRIOR FILING DATE: 2004-08-20
PRIOR FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 96
SSCOTAMRE: Patentin version 3.2
SEQ ID NO 81
LENGTH: 778
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APPLICANT: Casman, Stacie
APPLICANT: Boldog, Perence
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
TITLE REPRENCE: 21042-251
CURRENT PILING DATE: 2002-01-25,897
PRIOR PILING DATE: 2001-01-19
PRIOR PILING DATE: 2001-01-19
PRIOR PILING DATE: 2001-01-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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29.4%; Score 51.5; DB 6; Length 778;
Best Local Similarity 37.1%; Pred. No. 25;
Matches 13; Conservative 9; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INCOMENTION:
APPLICANT: DeCristociaco, Marc
APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Ballinger, Robert
APPLICANT: Ratelli, Luca
APPLICANT: Ratelli, Luca
APPLICANT: Ratelli, Luca
APPLICANT: Grow Ramesh
APPLICANT: Grows Ramesh
APPLICANT: Zerhusen, Bryan
APPLICANT: Zerhusen, Bryan
APPLICANT: Andrew, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baumgatrner, Jason
Shimkete, Richard
Gusev, Vladimir
Vernet, Corine
Paupler Jr., Raymond
Pena, Carol
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Mezes, Peter
Patturajan, Meera
Burgess, Cahterine
Eisen, Andrew
Wolenc, Adam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-505-263-81
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APPLICANT:
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Gaps

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| GENERAL INCOMMATION:
| JARBERAL INCOMMATION:
| APPLICANT: COHEN, Irun R. |
| APPLICANT: COHEN, Irun R. |
| APPLICANT: BESERWAN, Pierre |
| APPLICANT: BESERWAN, Pierre |
| APPLICANT: MOSONEGO, Alon |
| APPLICANTON INCOMENTED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES |
| FILE REFERENCE: ELS-SCHWARTZ-2A |
| CURRENT FILING DATE: 1990-128, 277 |
| PRIOR APPLICATION NUMBER: US 09/314,161 |
| PRIOR PLING DATE: 1990-12-22 |
| PRIOR PLING DATE: 1990-12-22 |
| PRIOR PLING DATE: 1990-07-21 |
| PRIOR FILING DATE: 1990-07-21 |
| PRIOR FILING DATE: 1990-12-1 |
| PRIO
Sequence 23, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 197583,
Sequence 242884,
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
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100.0%; Score 139; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 27; Conservative 0; Mismatches 0; Indels (
                      US-11-090-836-3
US-11-090-844-3
US-11-090-844-3
US-10-425-115-24284
US-10-425-115-24284
US-10-726-195-2
US-10-726-195-2
US-10-726-195-2
US-10-726-945-3
US-10-456-947-3
US-10-456-947-3
US-10-456-947-3
US-10-718-945-3
US-10-718-978-493-3
US-10-718-978-493-3
US-10-718-978-493-3
US-10-718-978-493-3
US-10-718-978-493-3
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US-10-718-978-493-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/09893348 Patent No. US20020072493A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-20
           09-893-348-20
           Sequence 20, Appl Sequence 164, Appl Sequence 18, Appl Sequence 19, Appl Sequence 10, Appl Sequence 10, Appl Sequence 24, Appl Sequence 3, Appl Sequence 9, Appli Sequence 9, Appli
                                                                                                                                          February 17, 2006, 03:57:08 ; Search time 97.6667 Seconds
(without alignments)
115.509 Million cell updates/sec
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1: /cgn2 6/ptcdata/l/pubpad/US07_PUBCOMB.pep:*
3: /cgn2 6/ptcdata/l/pubpad/US08_PUBCOMB.pep:*
4: /cgn2 6/ptcdata/l/pubpad/US10A_PUBCOMB.pep:*
4: /cgn2 6/ptcdata/l/pubpad/US10A_PUBCOMB.pep:*
5: /cgn2 6/ptcdata/l/pubpad/US10B_PUBCOMB.pep:*
6: /cgn2 6/ptcdata/l/pubpad/US10B_PUBCOMB.pep:*
                               GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-810-653-20
US-10-205-194-164
US-10-205-194-164
US-10-633-348-18
US-10-633-423-10
US-10-267-502-431
US-10-267-502-431
US-09-789-386-6
US-09-789-386-6
US-09-893-348-24
US-09-789-386-2
US-10-663-26
US-10-663-26
US-10-663-26
US-10-613-24
US-10-613-24
US-10-613-24
US-09-758-140-6
US-10-466-391A-9
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Maximum Match 100%
Listing first 45 summaries
                                                                                                          protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Sequence 20, Application US/10810653
Sequence 20, Application US/10810653
Publication No. US2040252218A1
GENERAL INPORMATION:
APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: BESENAN, Florre
APPLICANT: BESENAN, Plorre
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSURGO, Alon
TILE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

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RESULT 2 US-10-810-653-20

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RESULT 6
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US-10-205-194-164

| Sequence 164, Application US/10205194
| Publication No. US200303134301A1
| Publication No. US200303134301A1
| Publication No. US200303134301A1
| GENERAL INDEMENTION
| APPLICANT: Mee, Kevinhert Company
| APPLICANT: Dixon. Alistair
| APPLICANT: Brooksbank, Robert
| APPLICANT: Pinnock, Robert
| APPLICANT: Pinnock, Robert
| APPLICANT: Pinnock, Robert
| APPLICANT: WINABRIST (SOCOTOT-24)
| CURRENT FILING DATE: SOCO-07-24
| PRIOR APPLICATION NUMBER: GB 0118354.0
| PRIOR FILING DATE: 2000-07-27
| NUMBER OF SEQ ID NOS: 177
| SEQ ID NO 164
| EMBOTH: 379
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100.0%; Score 139; DB 5; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 27; Conservative 0; Mismatches 0; Indels C
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CURRENT APPLICATION NUMBER: US/10/810,653
CURRENT FILING DATE: 2004.03-29
FRIOR APPLICATION NUMBER: US/09/893,348
FRIOR FILING DATE: 2001.06-28
FRIOR FILING DATE: 1999-05-19
FRIOR FILING DATE: 1999-05-19
FRIOR PILING DATE: 1999-05-19
FRIOR APPLICATION NUMBER: US 09/218,277
FRIOR APPLICATION NUMBER: PCT/US98/14715
FRIOR APPLICATION NUMBER: PCT/US98/14715
FRIOR FILING DATE: 1998-12-22
FRIOR FILING DATE: 1998-12-19
FRIOR FILING DATE: 1998-15-19
FRIOR FILING DATE: 1998-05-19
FRIOR FILING DATE: 1098-05-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Foocen-m2 reticulon US-10-205-194-164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/09893348
Patent No. US2002007493A1
GENERAL INFORMATION:
APPLICANT: BISENBACH-SCHWARTZ, Michal
APPLICANT: COHEN, ITUN R.
APPLICANT: BESERVAN, PIETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Rattus norvegicus
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; ORGANISM: Rattus norvegicus
US-10-810-653-20
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US-09-893-348-18
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APPLICANT: WOSONEGO, Alon
APPLICANT: WOALEW, Gila
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES;
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES;
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US/09/893,348
CURRENT PELLING DATE: 1080-06-28
PRIOR PELLING DATE: 1999-05-19
PRIOR PELLING DATE: 1999-05-19
PRIOR PELLING DATE: 1998-07-21
PRIOR PELLING DATE: 1998-07-21
PRIOR PELLING DATE: 1998-07-21
PRIOR PELLING DATE: 1998-07-21
PRIOR PELLING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
SOUTHARE: PARCHAIN VERSION 3.1
SEQ ID NO 18
LENGTH: 1163
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US-10-810-653-18

US-10-810-653-18

Sequence 18, Application US/10810653

Publication No. US20040253218A1

GENERAL INFORMATION:

APPLICANT: COHEN, Irun R.

APPLICANT: COHEN, Irun R.

APPLICANT: COHEN, Irun R.

APPLICANT: MOALEN, Gila

TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

FILE REFERENCE: ELS-SCHWARTE2AA

CURRENT APPLICATION NUMBER: US/10/810,653

CURRENT APPLICATION NUMBER: US/10/893,348

PRIOR APPLICATION NUMBER: US/09/893,148

PRIOR APPLICATION NUMBER: US 09/218,177

PRIOR APPLICATION NUMBER: US 09/218,277

PRIOR PLING DATE: 1998-05-19

PRIOR PLING DATE: 1998-05-19

PRIOR PLING DATE: 1998-05-19

PRIOR PLING DATE: 1998-05-19

NUMBER OF SEQ ID NOS: 29

NUMBER OF SEQ ID NOS: 29

SEQOFWARE: Patentin Version 3.1

SEQUENCE: PATEOREMENT PATEOREME
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100.0%; Score 139; DB 5; Length 1163;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1163;
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; ORGANISM: Rattus norvegicus
US-10-810-653-18
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ORGANISM: Rattus norvegicus
US-09-893-348-18
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RESULT 10
US.09-765-205-6

Sequence 6, Application US/09765205

Sequence 10 Application US/09765205

Patent No. US20020034800A1

GENERAL INFORMATION:

APPLICANT: Cao, Li

TITLE DOF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES

FILE REFERENCE: 1458.004/200130.449

CURRENT PILING DATE: 1299-12.16

NUMBER OF SEQ ID NOS: 46

SOFTWARE: FRASEQ for Windows Version 3.0

SEQ ID NO 6

SEQ ID NO 6

TYPE REPERENCE: 133

TYPE RESERVENCE: 133

TYPE RESERVENCE: 133

TYPE RESERVENCE: 133

TYPE RESERVENCE: 133

US-09-165-205-6
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86.0%; Score 119.5; DB 4; Length 1163;
Best Local Similarity 92.6%; Pred. No. 0.00061;
Matches 25; Conservative 1; Mismatches 0; Indels 1;
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80.2%; Score 111.5; DB 3; Length 373;
Best Local Similarity 85.2%; Pred. No. 0.0013;
Matches 23; Conservative 3; Mismatches 0; Indels 1;
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80.2%; Score 111.5; DB 3; Length 373;

Best Local Similarity 85.2%; Pred. No. 0.0013;

Matches 23; Conservative 3; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-09-789-386-6
IS-09-789-386-6
Sequence 6, Application US/09789386
Patent No. US2002010324A1
GENERAL INFORMATION:
APPLICANT: MICHALOVICH, DAVID
APPLICANT: PRINNHA, RABINDER KUMAR
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REPERENCE: GP-30165-C1
CURRENT APPLICATION NUMBER: US/09/789,386
CURRENT APPLICATION NUMBER: US/09/789,386
CURRENT APPLICATION NUMBER: US/09/789,386
PRIOR APPLICATION NUMBER: US/09/789,386
PRIOR PELIGATION NUMBER: US/09/789,386
PRIOR PELIGATION NUMBER: US/09/789,386
PRIOR PELIGATION NUMBER: US/09/789,386
NUMBER: OF SEQ ID NOMBER: US/09/359,208
PRIOR PELING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 6

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                                                                                                                                                                                                                                                                                                                                                                             ; SOFTWARE: Patentin version 3.2; SEQ ID NO 43.1
; LENGTH: 1163
; TYPE: PRT
; TYPE: PRT
US-10-267-502-431
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; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-6
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Sequence 10, Application US/10427741

Sequence 10, Application US/10427741

Sequence 10, Application No. US20040191291A1

SEMERAL INFORMATION:

APPLICANT: Yemashita Toshihide

TITLE OF INVERTION: COMPOSITION AND METHOD FOR NERVE REGENERATION CURRENT PEPLICATION NUMBER: US/10/427,741

CURRENT PEPLICATION NUMBER: US/10/427,741

CURRENT PILING DATE: 2003-04-30

FRIOR APPLICATION NUMBER: JP 2003-92923

FRIOR PILING DATE: 2003-03-28

NUMBER OF SEQ ID NOS: 25

SOFTWARE PATENTIN VERSION 3.1

SEQ ID NO 10

LENGTH 1162
       Query Match
Best Local Similarity 92.6%; Pred. No. 0.00061;
Matches 25; Conservative 1; Mismatches 0; Indels 1;
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Best Local Similarity 92.6%; Pred. No. 0.00061;
Matches 25; Conservative 1; Mismatches 0; Indels 1;
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Publication No. US20040071700A1

GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
APPLICANT: Galant, Ron
TITLE OF INVENTION: Obesity Linked Genes
FILE REFERENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27

NUMBER OF SEQ ID NOS: 439
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; ORGANISM: Mus musculus
US-10-427-741-10
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US-10-267-502-431
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RESULT 13
US-10-408-50-8
US-10-408-50-8
Sequence 8, Application US/10408967
Publication No. US20040063161A1
GENERAL INFORMATION:
APPLICANT: Pan. Atqiang
APPLICANT: Van. Atqiang
APPLICANT: Lu. Yifeng
TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
FILE REFRENCE: 00925
CURRENT APPLICATION NUMBER: US/10/408,967
CURRENT FILING DATE: 2003-04-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE PATE: DATE: 2013-04-08
SEQ ID NOS: 9
SEG ID NO
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; Sequence 4, Application US/10466391A
; Publication No. US20040146953A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT PILICATION NUMBER: US/10/466,391A
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
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US-10-466-258-4
US-10-466-258-4
Sequence 4, Application US/10466258
Publication No. US20040132096A1
GENERAL INFORMATION:
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION:
FILE REPERENCE: P80966 GCV
CURRENT APPLICATION NUMBER: US/10/466,258
CURRENT FILING DATE: 2003-07-15
SOFTWARE: PETENTIN VOICE: 13
SOFTWARE: PETENTIN VOICE: 13
SOFTWARE: PETENTIN VOICE: 13
                                                      30 BPEDER-EREBEREDEDEDLERLEVL 55
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27
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; ORGANISM: Homo sapiens
US-10-408-967-8
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ORGANISM: Homo sapiens
US-10-466-258-4
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US-10-466-391A-4
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KESULT II.

KESULT II.

Sequence 24, Application US/09893348

Sequence 24, Application US/09893348

Sequence 24, Application US/09893348

Sequence 24, Application US/09893348

SEQUENCE 24.

APPLICANT: BESERAAN. Pierre

APPLICANT: BESERAAN. Pierre

APPLICANT: MOSUNEGO, Alon

CURRENT PRING DATE: 1999-05-19

PRIOR PILING DATE: 1999-05-19

PRIOR PILING DATE: 1998-05-19

PRIOR FILING DATE: 1998-07-21

PRIOR FILING DATE: 1998-05-19

PRIOR FILING DATE: 1998-05-19

PRIOR FILING DATE: 1998-05-19

NUMBER OF SEQ ID NOS: 29

SOFTWARE PATENTIN VERSION 3.1

SEQ ID NO 24

LENGTH: 373
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1 Similarity 85.2%; Pred. No. 0.0013;
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1/S-10-060-036-72
Sequence 72, Application US/10060036
Publication No. US20030073144A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Michael D.
APPLICANT: Persing, David H.
APPLICANT: Persing, David H.
APPLICANT: Persing, David H.
APPLICANT: Persing, David H.
APPLICANT: Jiang, Yuqiu T.
APPLICANT: Jiang, Yuqiu M.
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; LENGTH: 373
; TYPE: PRT
CORGANISM: Homo sapiens
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US-10-466-391A-4

BOL2*; Score 111.5; DB 4; Length 373;

Matches 23; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

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Search completed: February 17, 2006, 04:03:20
Job time: 97.6667 secs
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protein

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Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative giltoma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperpoliferative disorder; hanjan dysproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; diagnosis; structural plasticity; screening; mutant; mutein.
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastroma, medilloblastroma, craniopharyngioma, espendyoma, pinealoma, haemangioblastoma, accoustic neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and

Aay53624 Aay56969 Bab24242

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Result

Example; Page; 122pp; English.

Schwab ME,

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degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.

Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psorlasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is a fragment of rat Nogo A protein nebwn in AAVIJIO, which is used in the construction of mutean NAX. The mutant is composed of His-tag/T7-tag/vector/Nogo-A sequence as 1-171/vector. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory particularly amino acids 542-722. In addition, N-terminal region in the Nogo A sequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region to present sequence shown in AAVIJIO SEQ In numbers 53-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification.

The Mower, the specification does not include sequences for these SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperpoliferative disorder; banign dysproliferative disorder; banign dysproliferative disorder; pserionis; pseriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps

    17. 171
/note= "Corresponds to residues 1-171 of rat Nogo A protein shown in AAY71310"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 100.0%; Score 139; DB 3; Length 171; Similarity 100.0%; Pred. No. 1.4e-07; 27; Conservative 0; Mismatches 0; Indels 0
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S. E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 171 AA;
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(CHEN/) CHEN M
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The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth associated. Nogo proteins and fragments displaying neurite growth control activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, acoustic neuroma, craniopharyngioma, oligodendroglioma, menagioma, neuroblastoma acoustic neuroma in the promote Nogo activity can be used to transplationa and degenerative market diseases e.g. Alzheimer's and Parkinson's diseases. Therapputics which promote Nogo activity can be used to reat or prevent hyporproliferative or benign dysproliferative disorders e.g. pportasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit protocition of Nogo protein to induce regeneration of used to inhibit protocity of the CNS in disorders where neurons or to promote structural plasticity of the CNS in disorders where neurons or to promote structural plasticity of the CNS in disorders where an intended can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders and to screen for or test molecules which can treat or prevent disorders and to screen for or test molecules which can treat or prevent disorders and to screen for or test molecules which can treat or prevent disorders and to screen for or test molecules which can treat or prevent disorders and to screen for or test molecules which and the material is composed of His-Lag/Ty-Lag/Ty-CngOrder Agenence and 1-171 + and the construction of mutant is composed of His-Lag/Ty-Lag/Ty-CngOrder Agenence from mino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 in the sequence is predification but is derived from rat Nogo A sequence is not given in AA71310.

Specification but is derived from rat Nogo A sequen
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                                                                                         Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 100.0%; Score 139; DB 3; Length 359; Similarity 100.0%; Pred. No. 2.9e-07; 27; Conservative 0; Mismatches 0; Indels C
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                                                                                                                                                                   Example; Page; 122pp; English.
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                                           WPI; 2000-400052/34.
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Best Local Similarity
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The present sequence is a rat Nogo B protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) which in the present sequence of all central nervous system (CNS) transcript arises as a result of alternative splicing of Nogo gene. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, acoustic neuroma, oligodendroglioma, menagioma, hemangioblastoma and degenerative nerve disease e.g. neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. altheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benigm dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Thosymes or antisease Nogo nucleic acids can be used to inhibit correct structural plasticity of the CNS in disorders where neuring production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neuring models can be used in disquostic and screening methods for predisposition of disorders or disorder
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                                                                                                                                                                                                                                                                                  /note="Corresponds to C-terminal 188 amino acids (residues 976-1163) of Nogo A protein (AA771310). This residues 976-1163) of Nogo A, B and C isoforms" 185. 220
/label= Transmembrane domain /note= "C-terminal hydrophobic region"
                                          l. .171
'note= "Inhibits NIH 3T3 fibroblast spreading"
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/label= Transmembrane domain
/note= "C-terminal hydrophobic
/note= "Asn is N-glycosylated"
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286
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                                                                                                                                                 "Casein kinase II site"
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/note= "Asn is N-glycosylated"
270
protein shown in AAY71310"
                                                                                                                                                                                                                      "Acidic region"
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/note= "Ac
173. .360
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                                               Inhibitory-site
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The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central peripheral nervous system (NS). The method involves administering NS-specific activated T cells, NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, bunt trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or damages caused by surgery such as tumour excision. The disease is not an autolimume disease or neoplasm. The disease results in a degenerative process occurring in aither gray or white matter or both. The disease is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS; central nervous system; peripheral nervous system; tranquillizer; Nogo; vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant; nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy; neurotransmitter receptor; rat; receptor.
-1163 of Nogo A. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However the specification does not include sequences for these SEQ ID numbers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Promoting nerve regeneration and preventing neuronal degeneration in the central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or analogs/peptides.
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                                                                                                                    Length 360;
                                                                                                                  Match
Local Similarity 100.0%; Score 139; DB 3; Length 36
Local Similarity 100.0%; Pred. No. 2.9e-07;
Les 27; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                  ABB81076 standard; protein; 360
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98WO-US014715.
98US-00218277.
99US-00314161.
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N-PSDB; ABN86600.
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                                                                                     Sequence 360 AA;
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19-MAY-1999;
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21-JUL-1998;
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disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and than the deficiency, intervertebral disc herniation, prion diseases of the control of the season as Creuzfeldt-Jakob disease, acapal tunnel syndrome, peripheral control of the season in the season of th
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/note= "This region is common to Nogo A, B and
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note= "Inhibits NIH 3T3 fibroblast spreading"
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Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 27; Conservative 0; Mismatches 0; Indels C
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/label= Transmembrane domain
/note= "C-terminal hydrophobic region"
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269. .271
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/note= "Acidic region"
173. .361
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibitory-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
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The present sequence is an alternative version of rat Nogo B protein

C which is a potent neural cell growth inhibitor and is free of all central

c nervous system (CNS) myelin material with which it is natively

c associated. The Nogo B transcript arises as a result of alternative

c splicing of Nogo gene. Nogo proteins and fragments displaying neurite

c graniopharyngioma. Piplandama, heament of neoplastic

disease of the CNS e.g. glioma, pinealoma, neuroblastoma, acoustic

c raniopharyngioma, pepadyoma, pilolabatoma, neuroblastoma, acoustic

c raniopharyngioma, pepadyoma, pilolabatoma, neuroblastoma, acoustic

c raniopharyngioma, pepadyoma, pilolabatoma, neuroblastoma or rethioblastoma

and degenerative nerve diseases e.g. Alzheimer's and Parkinson's

c neuroma, oligodandroglioma, menagioma, neuroblastoma or rethioblastoma

c and degenerative nerve diseases e.g. Alzheimer's and Parkinson's

c provent hyperproliferative or benign dysproliferative disorders e.g.

c progratis and tissue hypertrophy. Ribozymes or antisense Nogo mucleic

c progratis and tissue hypertrophy. Ribozymes or antisense Nogo mucleic

c progratis and tissue hypertrophy. Ribozymes or antisense Nogo mucleic

c acids can be used to inhibit production of Nogo protein to induce

c cids can be used to inhibit production or Nogo protein to induce

c disorders where neurite growth, regeneration or maintenance are deficient

c disorders where neurite growth, regeneration or maintenance are deficient

c or desired The animal models can be used in diagnostic and creening

c molecules which can treat or prevent disorders or diseases of the CNS.

C Note: The present sequence is not given in the specification but is

c alternative version of the Nogo B sequence (see AAY11383) described in

the specification does not include sequences for these SEQ ID numbers

c claim 32 and SEQ ID No: 29 in disclosure of the specification. However
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      go proteins and nucleic acids useful for treating neoplastic disorders the central nervous system and inducing regeneration of neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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288 - 323
/label= Transmembrane domain
/note= "C-terminal hydrophobic region"
339. .341
/note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                    /note= "Protein kinase C (PKC) site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 139; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 EPEDEEDEEEEBDEEEDDEDLEELEVL 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US026160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0107446P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SCHW/) SCHWAB M E.
(CHEN/) CHEN M S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-400052/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 361 AA;
                                                                                                                                                                                                                                                                                                                                                      WO200031235-A2.
                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                            32-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schwab ME,
                                                                 Domain
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ADB85283
ID ADB8
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The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myolin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth associated. Nogo proteins and fragments displaying neurite growth conditions, pleasing, the treatment of neoplastic disease of inhibitory activity are used in the treatment of neoplastic disease of the CNS of glooms, menagiona, medulloblastoma, craniopharyngioma, opendyoma, pleasing, head acoustic neuroma, or prevent diseases e.g. Alzheimer's and Parkinson's diseases. Conditional menagional menagional pleasing acoustic neuroma or prevent hyperproliferative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent and tissue or benomed activity can be used to thibit production of Nogo protein to induce regeneration of Mogo protein to induce regeneration of meaninensors are deficient or desired. The neurons or to promote structural plasticity of the CNS in disorders where canimal models can be used in diagnostic and screening methods for prevent disorders or disagnostic and screening methods for treat or prevent disorders and to screen for or test molecules which creat or prevent disorders or disagnostic and screening methods for the construction of mutant NiAstr. The mutant is composed of His-tag/Tr-cag/vector/Nogo-A sequence as 1-974/Tr-tag. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory construction was identified in the Nogo A sequence from amino acids 172-974, present sequence is not given in the specification but in disclosure of the specification of the specification but in disclosure of the specification.

The structure of the specification does not include sequence for these SEQ ID mumbers, the specification does not include sequence for these SEQ ID
central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperpoliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins and nucleic acids useful for treating neoplastic disorders ne central nervous system and inducing regeneration of neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 100.0%; Score 139; DB 3; Length 974; Local Similarity 100.0%; Pred. No. 8.1e-07; Indels 0: A Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example, Page, 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   98US-0107446P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schwab ME, Chen MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-400052/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (SCHW/) SCHWAB M E. (CHEN/) CHEN M S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 974 AA;
                                                                                                                                                                                                                                           WO200031235-A2.
                                                                                                                                                                                                                                                                                                                                                  05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-1998;
                                                                                                                                                                                                                                                                                                  02-JUN-2000.
                                                                                                                                                                                                 Rattus sp.
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AAY71557
ID AAY7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel isolated gene sequence that is down-
cargulated in the spinal cord in response to streptozocin-induced
diabetes, or comprising, hybridising or having at least 0% sequence
cleantity to a sequence whose expression products are kinases,
dentity to a sequence whose expression products are kinases,
coupled receptor proteins, DNA-binding proteins, proceases or enzymes,
given in the specification. A gene of the invention has analgesic
activity, and may have a use in gene therapy. The gene sequences, vector,
host cell, animal, polypeptide and antibody are useful for screening of
compounds for diagnosing or treating pain. The kits are useful for
simultaneous, separate or sequence in the spinal cord of a mammal in response
to streptozocin-induced diabetes. The compound or pharmaceutical
composition is useful as a medicament for treating or diagnosing pain.
The present sequence represents a protein encoded by a gene of the
invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of gene sequence that is down-regulated in response to streptozocin-
induced diabetes, vector, host cell, animal, polypeptide and antibody, in
screening of compounds for treating or diagnosing pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat Nogo A protein fragment used in the construction of mutant NiAext.
                                                                                                                                                                         rat; streptozocin; kinase; phosphatase; ion channel protein; receptor; transporter; G-protein coupled receptor; GPCR; DNA-binding proteins; protease; enzyme; analgesic; gene therapy; pain; diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee K, Pinnock RD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 239-240; 256pp; English.
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                                                                                                                           Rat foocen-m2 reticulon SEQ ID NO:164.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-2002; 2002EP-00255228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUL-2001; 2001GB-00018354.
07-FBB-2002; 2002GB-00002880.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brooksbank RA, Dixon AK,
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WARN ) WARNER LAMBERT CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-364994/35.
N-PSDB; ADB85284.
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nes 27; Conserv
                                                                                                                                                                                                                                                                                   Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 379 AA;
                                                                                                                                                                                                                                                                                                                                EP1284297-A2.
                                                                           04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                       19-FEB-2003
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The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ce pendyoma, pinealoma, heamagioblastoma acoustic neuroma, craniopharyngioma, chisodendroglioma, menagioma, medulloblastoma or retinoblastoma and cilisodendroglioma, menagioma, encoblastoma or retinoblastoma and cilisodendroglioma, menagioma, encoblastoma or retinoblastoma and cilisodendroglioma, menagioma, the menagioblastoma or retinoblastoma and cilisodendroglioma, menagioma, praticipator or retinoblastoma and tissue hypertrophy. Ribozymes or tanicisons on ucleic acids can be can dissue hypertrophy. Ribozymes or tanicisons on ucleic acids can be can to promote structural plasticity of the CNS in disorders where neurons or to promote structural plasticity of the CNS in disorders where consult models can be used in disquostic are deficient or desired. The animal models can be used in disquostic are deficient or desired. The crast or prevent disorders and to screen for or test molecules which or treat or prevent disorders and to screen for or test molecules which crast or prevent disorders or diseases of the CNS. The present sequence taginate Nogo-A. Nogo-A sequence from which to supplied to minibitory sides of Nogo protein. Major inhibitory cognities of magning the inhibitory sides of Nogo protein. Major inhibitory can great on a deletion or and sequence shown in the Nogo-A. Nogo-A sequence from amino acids 172-722. In addition, N-terminal region 1-171 was hong a sequence shown in the specification but is derived from mumbers is an organized for mean and sequence shown in the specification or the specification does not include sequences for these SEQ ID mumbers, the specification does not include sequences for these sequences for mumbers is sequences.
                                                                                                                                          Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperpoliferative disoader, and another disease; parkinson's disease; pserviasis; tissue hypertophy; neuronal regenerative disorder; diagnosis; structural plasticity; screening; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nogo proteins and mucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
                                                                                                Rat Nogo A truncated protein used in the construction of mutant Nogo-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example, Page, 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0107446P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US026160
                                                              02-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schwab ME, Chen MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SCHW/) SCHWAB M E. (CHEN/) CHEN M S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-400052/34
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                                                                                                                                                                                                                                                                                                                                                                                                    WO200031235-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-1998;
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Rat, neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antibases gene therapy; neuroblastoma; menagioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperpoliferative disorder, benign dysproliferative disorder; dispensible phyenististic dispersible phyenicalististic hypertrophy; neuronal regeneration; treatment; structural plasticity; screening.
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/note= "used as immunogen to generate antibody AS 472"
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| Second of the continuity of the control o
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note= "Inhibits NIH 3T3 fibroblast spreading"
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/note= "Asn is N-glycosylated"
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542. .722
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note= "Asn is N-glycosylated"
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/note= "Asn is N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .58
.e= "Acidic region"
                                                                                                                                                                              Rat neurite growth inhibitor Nogo A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                     AAY71310 standard; protein; 1163 AA.
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100.0%; Score 139; DB 3; Length 1162;
Best Local Similarity 100.0%; Pred. No. 9.7e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                'note= "C-terminal common region found in Nogo A, B and C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to proteins and nucleic acids useful for treating neoplastic disorders the central nervous system and inducing regeneration of neurons.
                                                                                                                                                                                                  'note= "This region is not essential for inhibitory
                                                                                                                                                                                                                                                                                                                                                                            1090. .1125
/label= Transmembrane_domain
/dects= "C-terminal hydrophobic region specifically
/described in claim 16"
                                                                                                                                                                                                                                                             /label= Transmembrane domain
/note= "C-terminal hydrophobic region specifically
described in claim 16"
                                                                                                                                                                             note= "PKC and casein kinase II sites" 375. .1162
                                                                                                                                                                                                                                                                                                                                      /note= "Protein kinase C (PKC) site"
1089
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                   site"
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"Protein kinase C (PKC)
                   note= "Protein kinase C (PKC)
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                                       note= "Protein kinase C (PKC)
                                                         note= "Casein kinase II site"
                                                                                                          712. .914

note= "Asn is N-glycosylated"

725. .927

note= "Asn is N-glycosylated"
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note= "Asn is N-glycosylated"
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'note= "Asn is N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCHW/) SCHWAB M E. (CHEN/) CHEN M S.
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and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, candiloblastoma, acoustic neurona, oligodendreglioma, menagioma, hemangioblastoma, acoustic neurona, oligodendreglioma, menagioma, constituente neuronal expendioma, menagioma, menagioma, acoustic neuronal expendioma, menagioma, menagioma, acoustic neuronal expensional menagioma, menagioma, acoustic nettinoblastoma and degenerative nerve diseases e.g. Grativity can be used to treat or prevent hyperproliferative or benign disorders e.g. psoriasis and tissue hypertrophy.

C disproliferative disorders e.g. psoriasis and tissue hypertrophy.

CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit or production of Nogo protein to induce regeneration of neurons or to production of Nogo protein to induce regeneration of mentros or to growth, regeneration or maintenance are deficient or desired. The animal comparison of maintenance are deficient or desired. The animal comparison of disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence for or test molecules which can treat or consequence as SEQ ID No: 2 is stated to be the same as the sequence or referred in Claim 12 and SEQ ID No: 29 in disclosure of the sequences for preferred in Claim 12 and SEQ ID No: 29 in disclosure of the grounders of the sequences for these SEQ ID numbers
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hote= "There is Leu at this position in the sequence
shown in AAY71310"
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Anote= "Acidic region"
172. .259
Anote= "This region is not essential for inhibitory
activity"
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1. .171
/note= "Inhibits NIH 3T3 fibroblast spreading"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alternative version of rat neurite growth inhibitor Nogo A.
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/note= "Asn is N-glycosylated"
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Best Local &
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The present sequence is an alternative version of rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth associated. Nogo proteins and fragments displaying neurite growth cinhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pincaloma, haemangioblastoma and coligodendroglioma, menagioma, neuroblastoma and degenerative nerve diseases e.g. Alzhelmer's and Parkinson's diseases.

Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be neuron to promote structural plasticity of the CNS in disorders where neurite growth, responsation or maintenance are deficient or desired. The prevent profession of animal models can be used in disorders and screening methods for predisposition to disorders and to screen for or test molecules which can test or prevent disorders or disorders and correnting methods for predisposition to disorders and to screen for or test molecules which can sequence is an alternative version of the Nogo A sequence shown in Fig. A green ANTISHO. SEQ ID numbers 32-42 are referred in claim 32 and SEQ 1D NO: 29 in disclosure of the specification. However the specification or the sequences and the sequence is not include sequences for these SEQ ID numbers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
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                                                                                                                  region"
                    note= "Protein kinase C (PKC) site"
                                                         'note= "Protein kinase C (PKC) site"
                                                                                                                                                                                           /note= "Protein kinase C (PKC) site"
                                                                           1090. .1125
/label= Transmembrane domain
/note= "C-terminal hydrophobic
                                                                                                                                  1141. .1143
/note= "Asn is N-glycosylated"
1143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Schwab MB, Chen MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-400052/34.
                                                                                                                                                                                                                                                                                                                                                                                     (SCHW/) SCHWAB M E. (CHEN/) CHEN M S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1163 AA;
                                                                                                                                                                                                                                  WO200031235-A2
                                                                                                                                       Modified-site
Modified-site
                                    Modified-site
                                                                                                                                                                           fodified-site
                                                                                                                                                                                                                                                                                                           5-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                  16-NOV-1998;
                                                                                                                                                                                                                                                                         02-JUN-2000.
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                                                                             Domain
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  note= "C-terminal common region found in Nogo A, B and C soforms"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              762. .1163
/note= "used as immunogen to generate antibody AS Bruna"
                                                                                                                                                                                           /label= Unknown
//note= "There is Lys at this position in the sequence
shown in AAY71310"
                                                                                                                                                                                                                                                                                                                                                                                                                              623. .640
/note= "used as immunogen to generate antibody AS 472"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /notes "There is Asn at this position in the sequence shown in AAY71310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "There is Leu at this position in the sequence shown in AAY71310"
                                                         /note= "There is Ile at this position in the sequence shown in AAY71310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "This region is not essential for inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "PKC and casein kinase II sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "PKC and casein kinase II sites"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Protein kinase C (PKC) site"
1071. .1073
/note= "Asn is N-glycosylated"
                  /note= "Protein kinase C (PKC) site"
                                                                                                                  /note= "Protein kinase C (PKC) site"
                                                                                                                                                                                                                                                                       'note= "Protein kinase C (PKC) site"
                                                                                                                                                                                                                                                                                                              /note= "Protein kinase C (PKC) site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   694. .696
/note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Casein kinase II site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Casein kinase II site"
                                                                                                                                    168. .470
'note= "Asn is N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                  /note= "Casein kinase II site"
                                                                                                                                                                                                                                                                                                                                                                                                         note= "Casein kinase II site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Asn is N-glycosylated"
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. . . 914
/note= "Asn
?5. . 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88. .1023
label= Tra
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Modified-site
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Gaps 0;

The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering (NS-specific activated T cells, MS-specific antigen, its analogue or its perpetide, a mucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system of from injury/disease, where the injury is spinal cord injury, blunt from injury/disease, where the injury is spinal cord injury, blunt from injury/disease, where the injury is spinal cord injury, blunt from injury/disease, where the injury is spinal cord injury, blunt crawma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or damages caused by surgery such as tumour excision. The disease is not an autoimmunne disease or neoplasm. The disease results in a degenerative autoimmunum disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, camportrophic lateral sclerosis, non-arteritic optic neuropathy, and controperson's disease, including but not limited or vitamin deficiency, intervertebral disc herniation, prion diseases such as crawled signals, observations of whith various diseases, including but not limited camporate, observations of warious drawses, including but not limited camporate, observations of various drawses, accomplasion, observations of various drawses, including but not limited particles opportations of various drawses, accompally, malabsorption capacity and disease, accompally, malabsorption capacity engage (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia amplance approached and an example of NS-specific caparions in the present sequence represents the rate of an example of NS-specific central nervous system, peripheral nervous system, tranquillizer, Nogo, vulnerary, cerebroprotective, anti-tumour; antidabetic; anticonvulsant; nootropic; antiparkinsonian; ophthalmological; analgesic; hepstotropic; osteopathic; vasotropic; nephrotropic; cytostatic; analgesic hepstotropic; nephrotropic; cytostatic; analgesic hepstotropic; nephrotropic; cytostatic; antigen; gene therapy; neurotransmitter receptor; rat; receptor. Promoting nerve regeneration and preventing neuronal degeneration in the central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or analogs/peptides. Cohen IR, Beserman P, Mosonego A;

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The present invention relates to an isolated truncated Nogo-A polypeptide that corresponds to a truncated form of the Nogo-A protein from the rat and from the human. The truncated polypeptide is useful for identifying a compound having detectable affinity to a Nogo-A protein. The present sequence is a Nogo-A polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                    New isolated truncated Nogo-A polypeptide that corresponds to a truncated form of the Nogo-A protein, useful for identifying a compound having detectable affinity to a Nogo-A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                               rat; human; Nogo-A; truncated; affinity; membrane-bound protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 139; DB 8; Length 1163; 100.0%; Pred. No. 9.7e-07; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPEDEEDEEEEEEDEEDDEDLEELEVL 27
                                                                                    ADO26399 standard; protein; 1163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 6A; 80pp; English.
                                                                                                                                                           Rat truncated Nogo-A protein.
                                                                                                                                                                                                                                                                                 31-OCT-2002; 2002WO-EP012210.
                                                                                                                                                                                                                                                                                                          31-OCT-2002; 2002WO-EP012210.
                                                                                                                                                                                                                                                                                                                                 (PIER-) PIERIS PROTEOLAB AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                        Skerra A, Fiedler M;
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-376159/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1163 AA;
                                                                                                                                                                                                                                  WO2004039836-A1.
                                                                                                                                                                                                                                                          13-MAY-2004.
                                                                                                                                                                                                           Rattus sp.
                                                                                                             ADO26399;
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binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640; nerve repair; neuroprotective; gene therapy; central nervous system injury; CNS injury; neurodegenerative disorder;

Rattus norvegicus

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Gaps ö

Length 1163; Indels

Query Match
Best Local Similarity 100.0%; Pred. No. 9.7e-07;
Matches 27; Conservative 0; Mismatches 0;

Rat NogoA protein SEQ ID NO:26.

(first entry)

09-SEP-2004

ADP45572;

ADP45572 standard; protein; 1163 AA.

RESULT 13

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19-SEP-2003; 2003GB-00021997.
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                                                                                                                                                                                                                                                                   sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a binding molecule which binds to human Nogah polypeptide, human Nig, human Nig-D20 or human Nogah 623-640 with a dissociation constant of less than 1000pM. Also described: [1] a polymuclectide encoding the binding molecule; (2) an expression vector or system comprising the polymuclectide; (3) a host call comprising the expression system; (4) a pharmaceutical composition comprising the binding molecule and a carrier or diluent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence represents rat NogoA, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                         New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-
D20 or NogoA623-640, useful in preparing a composition for treating CNS
injury or neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody; NogoA; pharmaceutical; peripheral neuropathy; central nervous system disease; neurodegenerative disease; Jahlaniemera disease; Parkinsons disease; motor neurone disease; coular disease; diabetic retinopathy; age related macular degeneration; myopia; cns-gen; neuroprotective; nootropic; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                          Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;
Zurini M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 139; DB 8; Length 1163; 100.0%; Pred. No. 9.7e-07; rive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 26; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 BPEDEEDEERDEERDDEDLEELEVL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EPEDEEDEEEEDEEEDEDLEELEVL 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myopia; cns-gen; neuroprotectiv
antidiabetic; ophthalmological.
                                                                                                                             10-DEC-2002; 2002GB-00028832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-2004; 2004WO-EP010489.
                                                                                           09-DEC-2003; 2003WO-EP013960.
                                                                                                                                                             (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS PHARMA GMBH.
(UYZU-) UNIV ZUERICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat NogoA polypeptide.
                                                                                                                                                                                                                                                                                      WPI; 2004-468818/44.
N-PSDB; ADP45571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2005028508-A2.
                     WO2004052932-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUN-2005
                                                       24-JUN-2004.
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The invention relates to binding molecules (SEQ ID Nos 2 and 3) capable of binding to human NogaA polypeptide (SEQ ID No: 5), human NiG cof binding to human NogaA bolypeptide (SEQ ID No: 5), human NiG cof binding to human NogaA 342-357 (SEQ ID No: 6) all given in the specification, with a dissociation constant of less than 1000m. The binding molecule of the invention comparises a first antigen binding site comprising molecule of the hypervariable regions CDR-H1. CDR-H2, and CDR-H3, where each of the hypervariable regions CDR-H1. CDR-H2. and CDR-H3. Aber each of the hypervariable regions CDR-H1. Abor (SEQ ID No: 8), CDR-H2-A6 (SEQ ID No: 6), and CDR-H3-A6 (SEQ ID No: 10) all given in the specification, and a second antigen binding site comprising in sequence the hypervariable cregions CDR-L1, CDR-L2, and CDR-L3, and CDR-L2, and CDR-L3, and CDR-L2, and CDR-L3, and CDR-L3,
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                                                                                                                                                                                                                                                                                                                                                                                    New binding molecule capable of binding to human NogoA polypeptide, human
NiG, human NiG-D20, or human NogoA342-357, useful for treating nerve
repair, Alzheimer's disease, Parkinson's disease, or amyotrophic lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                             Schwab ME, Vitaliti A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 26; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RPEDEEDEEREDEERDDEDLEELEVL 27
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                                                                                                                                                                                  Barske C, Frentzel S, Mir AK,
(NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS PHARMA GMBH.
(UYZU-) UNIV ZURICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                           WPI; 2005-242564/25.
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                                                                                                                                                                                                                                                                                                                     N-PSDB; ADZ07608.
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The present invention relates to a method for regenerating nerves or medulating nerve regeneration. The method involves inhibiting or modulating as p75 signal transduction pathway. The invention is useful for treating, preventing or diagnosing neurological diseases based on nerve regeneration and for identifying agents useful for nerve regeneration. The invention is also useful in gene therapy and for preparing vaccine. The present sequence is the Mus musculus Nogo protein. Note: This sequence is said to encoded by SEQ ID NO 9, however this does not appear to be the same.
                                                                                                                                                                                                                                                                                                                                                                                                                 Regenerating nerves or modulating nerve regeneration comprises inhibiting or modulating p75 signal transduction pathway by administering a transduction agent, e.g. p21 or Rho, or an agent that interacts with the transduction agent.
                                        Nerve regeneration; gene therapy; vaccine; neuroprotective; nootropic; Nogo; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 86.0%; Score 119.5; DB 8; Length 1162; Best Local Similarity 92.6%; Pred. No. 0.00012; Matches 25; Conservative 1; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 10; 209pp; English.
                                                                                                                                                                                                                                  28-MAR-2003; 2003JP-00092923.
30-APR-2003; 2003US-00427741.
                                                                                                                                                                                                    31-JUL-2003; 2003US-00633423
                Mus musculus Nogo protein.
                                                                                                                                                                                                                                                                                                                                       Tohyama M, Yamashita T;
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-698659/68.
N-PSDB; ADT89536.
                                                                                                                                                                                                                                                                                     (TOHY/) TOHYAMA M. (YAMA/) YAMASHITA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1162 AA;
                                                                                                                                US2004191240-A1.
                                                                                                  Mus musculus.
                                                                                                                                                                  30-SEP-2004.
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Search completed: February 17, 2006, 03:49:29 Job time : 127.333 secs 31 EPEDEEDEEDEE - EEEDDEDLEELEVL 56 a

1 EPEDEEDEEEEDEEEDDEDLEELEVL 27

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1;

Gaps 1;

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February 17, 2006, 03:49:55; Search time 19:3333 Seconds (without alignments) (althout alignments) 1343.372 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                          US-09-830-972A-2_COPY_31_57
139
1 EPEDEEDEEEEEDEEEDDEDLEELEVL 27
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Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote hypothetical prote probable immediate hypothetical prote heat shock related nonhistone chromos troponin T - fruit troponin T - fruit troponin T - fruit de RNAl protein homol RNAl protein homol oncoprotein ze-Myc nonhistone chromos nonhistone chromos hypothetical prote immunophilin FKBP4 protein T27G7.4 [i glutamic acid-rich nucleolin - chicke myelin transcripti SUMMARIES 830221 NSH0H2 NSH0H2 NSH714 NSH0H2 NS * Query Match Length DB Score Result No.

ryanodine receptor nonhistone chromos high-mobility grou high mobility grou nonhistone chromos nonhistone chromos hypothetical prote

nucleolin - Chines hypothetical prote nonhistone chromos	hypothetical prote nonhistone chromos non-histone chromo	nucleosome assembl probable resistanc	nucleolin - mouse nucleolin - human nucleolin - rat	hypothetical prote hypothetical prote	delca-crystallin/s hypothetical prote Na+/Ca2+,K+-exchan
A27441 T33074 A27853	B71446 NSRTH1 148688	S60892 F71437	DNMS A35804 JH0148	S65169 S52522	JC4934 T12529 S20969
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30 31	1 6 9 6 1 6 4 6	36	ω ω 4. Θ φ Ο	4.4.	44 44 5

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nonvication chromosomal protein HMG-2B - human (fragment)
C;Bpecies: Homo sapiens (man)
C;Bpecies: Homo sapiens (man)
C;Bpecies: Homo sapiens (man)
C;Bpecies: 22-Nov1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: 530021
R;Alexandre, S.; Li, W.W.; Lee, A.S.
Nucleic Acids Res. 20, 6413, 1992
Nucleic Acids Res. 20, 6413, 1992
A;Itle: A human HMG2 ChMA with a novel 3'-untranslated region.
A;Ricession: 530021; MUID:93117123; PMID:1475204
A;Accession: 530021
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Accession: Signal NUIPROT:P26583; UNIPARC:UPIONOO16AA6C; EMBL:217240; NID:931334; PIDN: A;Residues: 1-166 ALE>
A;Cress-references: UNIPROT:P26583; UNIPARC:UPIONOO16AA6C; EMBL:217240; NID:931334; PIDN: A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Kayords: chromosomal protein (fragment) < HMG>
F;1-60/Domain: HMG box homology (HMG)>
F;69-143/Domain: HMG box homology < HMG)>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Northistone chromosomal protein HMG-2 - human
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Ja.Mar-1992 #sequence revision 31-Mar-1992 #text_change 09-Jul-2004
C.Accession: A42425; S20061; $18068
R.Shirakawa, H.; Yoohida, M.
J. Biol. Chem. 267, 6641-6645, 1992
A.File: Structure of a gene coding for human HMG2 protein.
A.File structure of a gene coding for human HMG2 protein.
A.File structure of a gene coding for human HMG2 protein.
A.File structure of a gene coding for human HMG2 protein.
A.File structure of a gene coding for human HMG2 protein.
A.File structure of a gene coding for human HMG2 protein.
A.File structure of a gene coding for human HMG2 protein.
A.File sequence extracted from NGB backbone (NCBIN:89899, NCBIP:89900)
A.File sequence extracted from NGB backbone (NCBIN:89899, NCBIP:89900)
A.File sequence of human HMG2 cDNA.
A.File sequence of human HMG2 cDNA.
A.File sequence of human HMG2 cDNA.
A.File ference number: S20061; MUID:92093633; PMID:1754403
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69.8%; Score 97; DB 2; Length 186;
Best Local Similarity 73.9%; Pred. No. 0.022;
Matches 17; Conservative 5; Mismatches 1; Indels
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A; Molecule type: mRNA
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Gaps

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probable immediate early protein - alcelaphine herpesvirus 1
C;Species: alcelaphine herpesvirus 1
C;Species: alcelaphine herpesvirus 1
C;Species: 24 Mar.1999 #sequence_revision 24-Mar.1999 #text_change 09-Jul-2004
C;Date: 24 Mar.1999 #sequence_revision 24-Mar.1999 #text_change 09-Jul-2004
C;Accession: T03166
R;Ensser, A.; Pflanz, R.; Pleckenstein, B.
J. Virol. 71, 6517-6525, 1997
A;Fitle: Primary structure of the alcelaphine herpesvirus 1 genome.
A;Reference number: Z14840; MUID:97404659; PMID:9261371
A;Reference number: T03166
A;Ateus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1300 ~ENS
A;Cross-references: UNIPROT:036421; UNIPARC:UP100000F856C; EMBL:AP005370; NID:92337967; I
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hypothetical protein R11A5.1a - Caenorhabditis elegans

C; paceles: Caenorhabditis elegans

C; pacels: Caenorhabditis elegans

C; pacession: T24166

C; Accession: T24166

A; Reference number: Z19848

A; Accession: T44166

A; Reterence number: Z19848

A; Molecule type: DXA

A; Molecule type: DXA

A; Residues: 1-906 < WIL>
A; Cross-references: UNIPROT:045718; UNIPARC:UPI0000083395; EMBL:Z83122; PIDN:CAB05598.1;

A; Experimental source: clone R11A5

C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Approchastical protein R11A5.1b - Caenorhabditis elegans
CiSpecies: Caenorhabditis elegans
CiSpecies: Caenorhabditis elegans
CiSpecies: Caenorhabditis elegans
CiSpecies: Tacc1.1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CiAccession: T24169
R;McMurray, A.
S;McMurray, A.
S;McMurray, A.
S;McMurray, A.
S;McGense number: Z19848
A,Reference number: Z19848
A,Reference number: Z19848
A,Reference number: T24169
A,Reference number: DNA
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Wolecule type: DNA
A,Status: DNA
A,Kenser-references: UNIPROT:062348; UNIPARC:UPI000007DBCA; EMBL:Z83122; PIDN:CAB05601.1;
A,Experimental source: clone R11A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 63.0%; Pred. No. 0.25;
Matches 17; Conservative 7; Mismatches 3; Indels
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A;Gene: (CSSP:R11A5.1b
A;Map position: 1
A;Introns: 14/2; 40/3; 277/3; 308/3; 353/3; 550/1; 658/1; 798/3
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C;Species: Mus musculus (house mouse)
C;Accession: S54774; S52211
R;Zwilling, S.; Koenig, H.; Wirth, T.
EMGO J. 14, 1199-1208, 1955
A;Title: High mobility group protein 2 functionally interacts with the POU domains of oc A;Title: High mobility group protein 2 functionally interacts with the POU domains of oc A;Title: High mobility group protein 2 functionally interacts with the POU domains of oc A;Title: High mobility group protein 2 functionally interacts muscularly A;Status: S54774
A;Status: preliminary; nucleic acid sequence not shown
A;Coss-references: UNIPROT: P30681; UNIPARC: UPIO00016432C; EMBL: Z46757; NID: g609168; PID C;Superfamin: HMG box homology <HMG1>
F;6-83/Domain: HMG box homology <HMG2>
F;9-166/Domain: HMG box homology <HMG2>
A;Residues: 1-209 <MAJ>
A;Cross-references: UNIPARC:UPI000013E34D; EMBL:X62534; NID:g32332; PIDN:CAA44395.1; PID
A;Cross-references: UNIPARC:UPI000013E34D; EMBL:X62534; NID:g32332; PIDN:CAA44395.1; PID
C;Geneticos:
A;Gene: GDB:NHCP2
A;Gross-references: GDB:119451; OMIM:118880
A;Gross-references: GDB:119451; OMIM:118880
C;Superfamily: nonhistone chromosomal protein HWG-2; HWG box homology
C;Keywords: Gixomosomal protein; DMA binding; nucleus
F;F.83/Domain: HWG box homology <HWG1>
F;92-166/Domain: HWG box homology <HWG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appointerical protein 48 - atelline herpesvirus 3 (strain 73)
Cypecides: atelline herpesvirus 3
Cybacides: atelline herpesvirus 3
Cybate: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
Cybacession: T4298
Cybacession: T4298
Cybacession: T4298
Cybaceston: T4298
Cybaceston: primary structure of the herpesvirus ateles genome.
Aybescription: Primary structure of the herpesvirus ateles genome.
Aybescription: T42963
Aybecession: T42964
Aybecession:
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Species: ateline herpesvirus 3
Variety: atrain 73
'Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 69.8%; Score 97; DB 1; Length 209; Best Local Similarity 73.9%; Pred. No. 0.025; Matches 17; Conservative 5; Mismatches 1; Indels
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Best Local
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Gaps

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**RiPythergy 1: 19.241; $4.745

5. Mol. Biol. 216, 657-675, 1990

7. Mol. Biol. 216, 657-675, 1990

8. Fightle: Drosophila melanogaster troponin-T mutations engender three distinct syndromes c A; Richtle: Drosophila melanogaster troponin-T mutations engender three distinct syndromes c A; Reference number: 813251; MUID:91080155; PMID:2124273

A; Rocession: 813251; MUID:91080155; PMID:2124273

A; Rocession: S13551

A; Rocession: S13551

A; Rocession: S29482

A; Reference number: S29482

A; Rocession: S29482

A; Rocession: S29482
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Nylternate names: calcium-release channel protein; junctional channel complex
Cispecies: Oryctolague cuniculus (domestic rabbit)
Cispecies: Oryctolague cuniculus (domestic rabbit)
Cipacesion: S04654; B35041; Ā36181; S53794; S32504
C; Accession: S04654; B35041; Ā36181; S53794; S32504
R; Taksbahlau, H.; Nibhimura, S.; Matsumoto, T.; Ishida, H.; Kangawa, K.; Minamino, N.; Mat
Nature 339, 439-445, 1989
A;Title: Primary structure and expression from complementary DNA of skeletal muscle ryanc
A;Reference unuber: S04654
A;Accession: S04654
A;Molecule type: mRNA
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 16-Feb-1997
C;Accession: S02708
R;Bullard, B; Leonard, K.; Larkins, A.; Butcher, G.; Karlik, C.; Fyrberg, E.
J. Mol. Biol. 204, 631-637, 1988
A;Fitle: Troponin of asynchronous flight muscle.
A;Reference number: S02708; MUID:89141761; PMID:2852258
A;Accession: S02708
A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Residues: 1-387 eBUL
A;Residues: 1-387 eBUL
A;Const. 2010
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A;Mesidues: 1-191,'A',193-396 <FYR2>
A;Cross-references: UNIPARC:UP10000137662; EMBL:X54504; NID:98739; PID:98740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          troponin T - fruit fly (Drosophila melanogaster)
CrSpecies: Drosophila melanogaster
Criste: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
CrAccession: S13251; S29482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 387;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 90; DB 2;
Pred. No. 0.18;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 EEEDEEDEEDEEEEEEEEEE 372
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A, Generics: Typase:up
A, Cross-references: FlyBase:FBgn0004169
A, Map position: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: FlyBase:up
A;Cross-references: FlyBase:FBgn0004169
C;Keywords: muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 68.0%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heat shock related protein - Plasmodium berghei
C;Species: Plasmodium berghei
C;Accession: T10455
R;Wiser, M.F.; Jennings, G.J.; Upparanukraw, P.; van Belkum, A.; Doorn, L.J.; Kumar, N.
R,Jritle: Purther characterization of a 58 kba Plasmodium berghei phosphoprotein as a coc
A,Reference number: Z17026; MUID:97164116; PMID:9010839
A,Accession: T10455
A,Accession: T10455
A,Rocession: T10455
A,Rocession: UNIPAC: UNIPAC: UNIONO016BF72; EMBL:L04508; NID:g309691; PIE
A,Experimental source: strain ANKA
C;Keywords: molecular chaperone
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// Status: preliminary
// Molecule type: mRNA
// Mosidues: 1.210 **MINA
// Statuses: 1.210 **MINA
// Statuses: 1.210 **MINATOR** INTO **
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
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                                  A,Gene: CESP:R11A5.1a
A,Map position:
A,introns:14/2, 40/3, 277/3; 318/3; 363/3; 560/1; 668/1; 808/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 92; DB 2; Length 376;
Pred. No. 0.12;
8; Mismatches 3; Indels
                                                                                                                                                                                Length 906;
                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                            Query Match 66.9%; Score 93; DB 2; Best Local Similarity 68.0%; Pred. No. 0.22; Matches 17; Conservative 5; Mismatches
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Best Local Similarity 59.3%;
Matches 16; Conservative
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RESULT 14
A3683
RNA1 homolog fug1 - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: A3698
RNA1 homolog fug1.
C; Accession: A36983
R; Requence_revision 06-Jan-1995 #text_change 09-Jul-2004
C; Accession: A36983
A; Title: A murine homolog of the yeast RNA1 gene is required for postimplantation develog A; Reference mumber: A36983; MUD:94148219; PMID:8314081
A; Reference muscal probleminary
A; Rocession: A36983
A; Residues: 1-589 cDEG>
A; Residues: 1-589 cDEG>
A; Residues: 1-589 cDEG>
A; Residues: Loss comes: UNIPROT:P46061; UNIPARC:UPI00000295A7; GB:U08110; NID:g472851; PIDN:}
C; Ganetics:
C; Ganetics:
C; Ganetics:
A; Map position: 15
C; Superfamily: Ran GTPase-activating protein (RanGAP) involved in mRNA processing and tre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oncoprotein zc-Myc - zebra fish
c)Species: Brachydanio rerio (zebra fish)
c)Species: Brachydanio rerio (zebra fish)
c)Species: 21.-3nn-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C)Accession: A48059
E)Accession: A48059
Mol. Cell. Biol. 13, 2765-2775, 1993
A)Title: Zebra fish myc family and max genes: differential expression and oncogenic actival, Recession: A48059; MUID:93233639; PMID:8474440
A)Accession: A48059
A)Accession: 
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A;Note: sequence extracted from NCB1 backbone (NCBIP:129810)
A;Note: sequence extracted from NCB1 protein; myc transforming protein homology
P;14-405/Domain: myc transforming protein homology <MYC>
Mol. Cell. Biol. 15, 2117-2124, 1995
A,Title: Separate domains of the Ran GTPase interact with different factors to regulate 1, A,Title: Separate domains of the Ran GTPase interact with different factors to regulate A,Reference number: 225932, MUID:95198731; PMID:7891706
A,Accession: T52070
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Roblecule Yppe: mRNA
A,Residues: 1-589 cREN
A,Gross-references: UNIPROT:P46061; UNIPARC:UPI000016CBOC; EMBL:U20857; PIDN:AAB60517.1
A,Experimental source: strain BALB/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: Fugi
A,Map poolation: 15
C,Superfamily: Ran GTPase-activating protein (RanGAP) involved in mRNA processing and
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64.0%; Score 89; DB 2; Length 589;
Best Local Similarity 69.6%; Pred. No. 0.34;
Matches 16; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 64.0%; Score 89; DB 2; Length 589; Local Similarity 69.6%; Pred. No. 0.34; Local es 16; Conservative 5; Mismatches 2; Indels
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Best Local Similarity
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Ry Varsanyi, M.; Meyer, H.E.

Biol. Chem. Hoppe-Seyler 376, 45-49, 1995

A.; Title: Sarcoplasmic reticular Ca(2+) release channel is phosphorylated at serine 2843

A.; Title: Sarcoplasmic reticular Ca(2+) release channel is phosphorylated at serine 2843

A.; Accession: 853794; MUID:95336639; PMID:7612188

A.; Molecule type: procedin

A.; Molecule type: Drocedin

A.; Molecule type: Molecule type: MID:89345969; PMID:8097730

A.; Ry Takebilma, A.; Mishimura, S.; Nishi, M.; Ikeda, M.; Sugimoto, T.

FEBS Lett. 322, 105-110, 1993

A.; Reference number: $32504; MUID:93245969; PMID:8097730

A.; Reference number: $32504; MUID:932
                                                                      A; Residues: 1-5037 <TAK>
A; Cross-references: UNIPROC::P11716; UNIPARC::UP1000013C4CA; EMBL:X15750; NID:g1709; PIDN:
A; Cross-references: UNIPROC::P11716; UNIPARC::UP1000013C4CA; EMBL:X15750; NID:g1709; PIDN:
A; Note: part of this sequence was confirmed by protein sequencing
A; Note: part of this sequence was confirmed by protein sequencing
A; Note: Did Comb.
A; Title: Molecular cloning of cDNA encoding human and rabbit forms of the Ca(2+) release
A; Reference number: A35041 MUID:90130482; PMID:2298749
A; Reference number: A35041 MUID:90130482; PMID:2298749
A; Residues: not compared with conceptual translation
A; Residues: 1-66, Y', 68-2014, 'D', 2016-3246, 'E', 3248-3480, 3486-4497, 'LE', 4498-4521, 'Q', 45
A; Residues: note: Compared with conceptual translation
A; Residues: 1-66, Y', 68-2014, 'D', 2016-3246, 'E', 3248-3480, 3486-4497, 'LE', 4498-4521, 'Q', 45
A; Residues: note: US, A: 86, 8683-8687, 1899
A; Title: Nolecular cloning and characterization of the ryanodine receptor/junctional characterization of the ryanodine receptor/junctional characterization of the A; Reference number: A36181; MUID:90046857; PMID:2813419
A; Retarus: nucleic acid sequence not shown; not compared with conceptual translation
A; Realise: mucleic acid sequence not shown; not compared with conceptual translation
A; Realise: mucleic acid sequence not shown; not compared with conceptual translation
A; Realise: MOID:90046857; PMID:2813419
A; Realise: mucleic acid sequence not shown; not compared with conceptual translation
A; Realise: MOID:90046857; PMID:2813419
A; Realise: MOID:90046857; PMID:280474700 cMAR>
A; Coss-references: UNIPARC:UP10000177941; UNIPARC:UP10000177942;
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RNA1 protein homolog Fug1 [imported] - mouse
Cippedies: Mus musculus (house mouse)
Cippedies: 20-0cct-2000 #sequence_revision 20-0ct-2000 #text_change 09-Jul-2004
Cipacesion: T52070
Cipacesion: T52070
W.; Clarke, M.; Villamarin, A.; Chi, A.; Coutavas, B.; Moore, M.S.; LoCurcio, M.; Clarke, V.
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Best Local Similarity 72.0%; Pred. No. 2.1;
Matches 18; Conservative 3; Mismatches 4; Indels
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Search completed: February 17, 2006, 03:56:51 Job time: 21.3333 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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Maximum Match 100%
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RY INCLEMENTAL SHORMS AND FORCE AND STATEMENT AND SACURANCE.

REALINE 2238857, PUMPED-12477912; DOI=10.1073/PDRS.242603899;

REDINE 2238857, PUMPED-1247. Grouse L.H., Derge J.G.,

RA Strausberg R.L., Felingold E.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechnol L.W. Marusina K., Parmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

RA Sapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabb B.R.,

RA Nilling M., Madan A., Sodergren E.J., Lu X., Gibbs R.A.,

RA Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W. Touchman J.W., Green E.D., Dickson M.C.,

RA Retried Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
                                                                                cryptospori
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Mammalia; Eutheria; Chordata; Craniata; Glires; Rodentia; Sciurognathi;
Muroldea; Muridea; Murinae; Rattus.
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NUCLECTIDE SEQUENCE.
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MEDILINE=22715687; PubMed=12832288;
Octlle T., Klinger M., Stuermer C.A., Schwab M.E.;
Octlle T., Klinger M., Stuermer C.A., Schwab M.E.;
"A reticular rhappody; phylogenic evolution and nomenclature of the
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Last annotation update)
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(961796_TBODU
(961095_XBULA
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(955C054_CRYPU
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NIH MGC Project;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota, Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
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( MEDLINE-22715887; PubMed=12832288; MEDLINE-22715887; PubMed=12832288; MEDLINE-22715887; PubMed=1283288; Moetule T., Kilnger M., Stuermer C.A., Schwab M.E.; Acticular rhapsody: phylogenic evolution and nomenclature of the TRIN/Nog gene family."; PASEB T. 17:1238-11247(2003).

IR PASEB T. 17:1238-11247(2003).

REMBL; AYL6411, ApA47316.1; -; mRNA.

REMBL; AYL6411, APA47316.1; -; mRNA.

REQUENCE 379 AA; 40719 MW; 9F15AB942D36EDOF CRC64;
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MEDLINE=223881257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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llarity 100.0%; Pred. No. 0.00019;
Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 100.0%; Score 139; DB 2; Length 360; Local Similarity 100.0%; Pred. No. 0.00018; Indels on 27; Conservative 0; Mismatches 0; 
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0708793 AAH70979.1; "RNA.
EMBL; ACK94744; AAH70979.1; "RNA.
EMBL; BC097936; AAH97936.1; "RNA.
GO; GO005793; C:endoplasmic reliculum; IEA.
InterPro; IPR003388; Reticulum; reliculum; PRA.
PRAM; PF02453; Reticulum; 1.
PROSTIE; PS50445; RETICULON; 1.
SEQUENCE 360 AA; 38622 MW; 149714AD6C3D65A7 CRC64;
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Rtn4 protein (Fragment).
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

Blatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,

Brangleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Ratagleton M.J., Used M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Ratagleton M.J., Used M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Ratagleton M.J., Willahy S.J.,

Ratagleton R.J., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbe R.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

Richards J., Halton E., Ketteman M., Rodrigues S., Sanchez A.,

Rhyting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Roderstation and initial analysis of more than 15,000 full-length human
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STRAIN-Sprague-Dawley; TISSUB-Adipocyte;
STRAIN-Sprague-Dawley; TISSUB-Adipocyte;
MUELINES-29449016; PubMed-10231557; DOI=10.1016/S0167-4889(99)00033-6;
MOTTIS N.J., Roses S.A., Reveu J.M., Lane W.S., Lienhard G.E.;
MOTTIS and Characterization of a 22 kDa protein from rat adipocytes:
a new member of the reticulon family. ";
Biochim. Biophys. Acta 1450:68-76(1999).
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COUNTIS; 09NUDS; 09NUDS; 09NUDS;

COUNTIS; 09NUTO;

COUNTIS; 09NUTO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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MEDLINE-20129255; PubMed=10667796; DOI=10.1038/35000219;
MEDLINE-20129255; PubMed=10667796; DOI=10.1038/35000219;
Spillman A.B., Whote A.B., Van der Haar M.E., Frank M., Schnell L., Spillman A.B., Christ F., Schwab M.E.; Frank M., Schnell L., Spillman A.B., Schwed M.E.; Frank M., Schnell L., Mogo-A is a myelin-associated neurite outgrowth inhibitor and antigen for monoclonal antibody IN-1.";
Nature 403:434-439(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 139; DB 2; Length 478; 100.0%; Pred. No. 0.00024; .ive 0; Mismatches 0; Indels (
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
Bubmit BC086375; AAH86375.1; -; mRNA.
NON TER 478 478
SEQÜENCE 478 AA; 51326 MW; B5A1B421A3541D2A CRC64;
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STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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AVLSAELSKTS -> MDGQKKHWKDK (in isoform

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                                              CONFLICT
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                                                                                                                                                                                                                                                  MEDILINE...

MEDILINE...

MEDILINE...

GrandPre T., Li S., Strittmatter S.M.;

GrandPre T., Li S., Strittmatter S.M.;

"Nogo-66 receptor antagonist peptide promotes axonal regeneration.";

Nature 417.547-551 (2002)

-1- FUNCTION: Potent neutite outgrowth inhibitor which may also help

block the regeneration of the nervous central system in adults (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R EMBL; AJ242961; CAB71027.1; -; mRNA.

R EMBL; AJ242961; CAB71027.1; -; mRNA.

R EMBL; AJ242962; CAB71029.1; -; mRNA.

R EMBL; AJ242963; CAB71029.1; -; mRNA.

R EMBL; AJ242963; CAB71029.1; -; mRNA.

R EMBL; AJ242064; AAD10109.1; -; mRNA.

R EMBL; AJ242065; CAB71020.1; -; mRNA.

R EMBL; AP130046; AAD10109.1; -; mRNA.

R EMBL; AP130046; AAD10109.1; -; mRNA.

R GO; GO:0010017; C:integral to endoplasmic reticulum membrane; IDA.

R GO; GO:0016021; C:integral to endoplasmic reticulum membrane; IDA.

R GO; GO:0005635; C:integral to endoplasmic reticulum membrane; IDA.

R GO; GO:0019997; P:incegral to endoplasmic reticulum membrane; ISS.

GO; GO:0019997; P:incegral to endoplasmic reticulum membrane; ISS.

R GO; GO:0019997; P:incegral to endoplasmic reticulum membrane; ISS.

R GO; GO:0019997; P:incegral to endoplasmic reticulum endoplasmic reticulum; ISS.

R InterPro; IPR003388; Reticulom; ISS.
                                                                                                                                                                                sintlatity)
-: SUBCELULIAR LOCATION: Integral membrane protein. Anchored to the
membrane of the endoplasmic reticulum through 2 putative
transmembrane domains (By similarity).
-: AltreRNATUR PRODUCTS:
                                                                                                                                      similarity).
-!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (in isoform 3).
/FTd=VSP_0656.
Missing (in isoform 2).
/FTd=VSP_06568.
Missing (in isoform 4).
/FTd=VSP_005659.
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Cytoplasmic (Potential).
Potential.
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PROSITE; PS50845; RETICULON; 1.
Alternative splicing; Direct protein sequencing; Endoplasmic reticulum; Transmembrane.
TOPO DOM 1 1989 Potential.
TOPO DOM 1011 1104 Lumenal (Potential).
TOPO DOM 1115 Potential.
TOPO DOM 1126 1125 Cytoplasmic (Potential).
TOPO DOM 1126 1163 Cytoplasmic (Potential).
TOPO DOM 1126 1163 Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mainly in the nervous system.
SIMILARITY: Contains 1 reticulon domain.
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964
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MEDINE=229/SvcJ7, Pubmed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
MEDINE=22976540; Pubmed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
Oertle T., Huber C., van der Putten H., Schwab M.E.;
"Genomic geructure and functional characterisation of the promoters of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamania; Eutheria; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                             Gaps
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Local Similarity 92.6%; Pred. No. 0.0082;
hes 25; Conservative 1; Mismatches 0; Indels 1;
                                                                                                              / Match 100.0%; Score 139; DB 1; Length 1163; Local Similarity 100.0%; Pred. No. 0.00054; Local Similarity 0; Mismatches 0; Indels 0;
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EMBL; AX102286; AAM73503.1; -; Genomic_DNA.
EMBL; AX102286; AAM73272.1; -; Genomic_DNA.
EMBLH, AX102286; AAM73272.1; -; Genomic_DNA.
EMBLH, ENSWORGGOO00020458; Mus musculus.
MGI:MGI1915835; Rtn4.
GO; GO:0043025; C:cell projection; IDA.
GO; GO:0005783; C:cell projection; IDA.
GO; GO:0005783; C:cell projection; IDA.
GO; GO:0005783; P:protein binding; IPI.
GO; GO:0005785; P:protein binding; IPI.
GO; GO:0001525; P:protein binding; IDA.
RO; GO:0001525; Regiculon.
R Pfam; PF0453; Reticulon; 1.
R PROSITE; PG0453; Reticulon; 1.
R PROSITE; PG045945; RETICULON; 1.
SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;
/Frid=VSP 005657.
1131 Missing (In Ref. 3; AAD31020).
A; 126388 MW; 8CB894B09E94F0B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/SvGJ7;
van der Putten H.;
Submitted (MAr-2002) to the EMBL/GenBank/DDBJ databases.
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van der Putten H., Mir A.;
Submitted (MAr-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
10-WAR-2005 (TrEMBLrel. 30, Last annotation update)
RTM4 (Reticulon 4).
Name=Rtn4, ORNames=RP23-17605.4-007;
Musmusculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                356 AA.
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J. Mol. Biol. 325:299-323(2003).
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QBBH78;
                                      1130 113
1163 AA;
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NUCLEOTIDE SEQUENCE.
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Manma-Ray,
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Musma-lai Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murines; Mus.
                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                             ch 86.0%; Score 119.5; DB 2; Length 375; 1 Similarity 92.6%; Pred. No. 0.0086; 25; Conservative 1; Mismatches 0; Indels 1;
                                                          Kay M.;

Kay M.;

Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; AX102286; AAM73504.1; -; mRNA.

EMBL; AX102286; AAM73504.1; -; Genomic DNA.

EMBL; AX102286; AAM73509.1; -; Genomic DNA.

EMBL; AX102286; AAM73509.1; -; Genomic DNA.

EMBL; AX102286; RAM4.

MOI: MGI.1915835; Rtn4.

MOI: MGI.1915836; Rtn4.

MOI: MGI.1915836; Reticulon.

Rtf-MY.1916945; Reticulon; I.

R PROSITE; RPO345; Reticulon; I.

R PROSITE; RO3306 MW; 23D9EB19BE671AE6 CRC64;
STRAIN=129SvcJ7;
Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                            31 BPEDEEDEEDEE-EEEDDEDLEELEVL 56
                                                                                                                                                                                                                                                                                                             1 RPEDEEDEEERDEEEDDEDLEELEVL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6; TISSUE=Brain;
                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
NUCLEOTIDE
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Q7TNB7 MOUSE
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Matches
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Koga H.;
"Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene.
"Prediction of the Coding Sequences of Mouse KIAA-homologous CDNAs
Identified by Screening of Terminal sequences of CDNA Clones Randomly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Motazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Ammalia; Eutheria; Euteria; Eurechontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Eurchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NOCBI _TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Fetal brain;
Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Nagase T., Ohara O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

86.0%; Score 119.5; DB 2; Length 1163;
Best Local Similarity 92.6%; Pred. No. 0.024;
Matches 25; Conservative 1; Mismatches 0; Indels 1;
                      DB 2; Length 1162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003388; Reticulon.
Pfam, PP02453; Reticulon; 1.
PROSITE; PS50845; RETICULON; 1.
SEQUENCE 1163 AA, 126690 MW; 6B5F362799417EA4 CRC64;
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jin W., 1000 M., Li R., Ju G.; Submittenanch, Li R., Ju G.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AY114152; AAM77068.1; -; mRNA. MRJ. MG1.1915835; Rtn4. GO; GO:00442955; C:cell projection; IDA. GO; GO:0043025; C:cell some; IDA. GO; GO:006783; C:cell some; IDA. GO; GO:0005152; P:protection binding; IPI. GO; GO:0001525; P:maglogenesis; IMP. GO; GO:0001252; P:meurogenesis; IDA.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
MKIAA4153 protein (Fragment)
NamesRtn4, Synonyme=mKIAA4153;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
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                  Query Match

86.0%; Score 119.5; DB

Best Local Similarity 92.6%; Pred. No. 0.024;

Matches 25; Conservative 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1163 AA.
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                                                                                                                                                                              1 EPEDEEDEEEEDEEDDEDLEELEVL 27
                                                                                                                                                                                                                                RESULT 11

OSDTK9 MOUSE PRELIMINARY;
AC OSDTK9
DT 10-MAY-2005 (TTEMBLrel. 30, pr. MAY-2005 (TTEMBLrel. 30, pr. MAY-2005)
CC ENKARYOCA: Metazoa (Chordata OC MARMALIa; Eutheria; Euarchon OC MAY-2004)
CC NCBI_TAXID=10090;
CC NCBI_TAXID=100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QBK3G8 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
NUCLEOTIDE SEQUENCE.
STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
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STRAIN=129/SvcJ7, and 129SvcJ7;
October 12, Huber C., van der Putten H., Schwab M.E.;
Nedenomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4.",
Nol. Biol. 325:299-331(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBEGM9_MOUSE PRELIMINARY; PRT; 1162 AA.
QBEGM9_MOUSE PRELIMINARY; PRT; 1162 AA.
QBEGM9_GBEGM9.
QBEGM9.
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KRAY M.;
Submitted (FEB-2005) to the EWBL/GenBank/DDBJ databases.

BWBL; AX102286; AAM73501.1; "; Genomic DNA.

EWBL; AX102286; AAM73511.1; "; Genomic DNA.

EWBL; AX102286; AAM73511.1; "; Genomic DNA.

ERSEMPL; ENSWIGGOOO0002048; Mus musculus.

MGI: MGI: MGI: 1918435; Rtn4.

GO; GO: 00043025; C:cell soma; IDA.

GO; GO: 0005783; C:endoplasmic reticulum; IDA.

GO; GO: 0005783; C:endoplasmic reticulum; IDA.

GO; GO: 0005783; P:endoplasmic reticulum; IDA.

GO; GO: 0005785; R:endoplasmic reticulum; IDA.

GO; GO: 0005785; R:endoplasmic reticulum; IDA.

FO; GO: 0007399; P:endoplasmic reticulum; IDA.

GO; GO: 0007399; R:eticulon.

FROSTITE: PF02453; Reticulon.

FROSTITE: PF02453; Reticulon.

FROSTITE: PF02453; Reticulon.

FROSTITE: PF02454; RETICULON.

FROSTITE: PF02454; RETICULON.

FROSTITE: PF02454; RETICULON.

FROSTITE: PF02454; RETICULON.
Strausberg R.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases. Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases. Bubmit BCG6373; AMH56373.; -; mRNA. MGI; MGI:1915835; Rtn4. GO; GO:0042995; C:cell projection; IDA. GO; GO:0005783; C:cell soma; IDA. GO; GO:0005783; C:cell soma; IDA. GO; GO:0005185; F:proteban binding; IPI. GO; GO:0001525; P:anglogenesis; IMP. GO; GO:0007399; P:neurogenesis; IDA.
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Van der Putten H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
TRAIN-1298/vcJ7;
Van der Putten H., Mir A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                 l protein.
720 Aa; 77435 MW; 80AB78728F16EAB2 CRC64;
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
SEQUENCE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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Gaps

Created) Last sequence update) Last annotation update)

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Q7L7Q6;
05-UL-2004 (TrEMBLrel. 27, Cx
05-UL-2004 (TrEMBLrel. 27, Le
10-MAY-2005 (TrEMBLrel. 30, Le
RTM4 isoform B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 HUMAN
Q96B16 HUMAN PRELIMINARY;
Q96B16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                          Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Best Local S:
Matches 23
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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80.2%; Score 111.5; DB 2; Length 185;
Best Local Similarity 85.2%; Pred. No. 0.022;
Matches 23; Conservative 3; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.0%; Score 119.5; DB 2; Length 1245; 92.6%; Pred. No. 0.026; Live 1; Mismatches 0; Indels 1;
Sampled from Size-Fractionated Libraries..";
L Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
E EMBL; AK22611; BAD90301.1; -; mRNA.
R MGI; MGI:1916345; Rtn4.
R GO; GO:0043025; C:cell Soma; IDA.
R GO; GO:0043025; C:cell Soma; IDA.
R GO; GO:005515; F:protein binding; IPI.
R GO; GO:005515; P:protein binding; IPI.
R GO; GO:00515; P:protein binding; IPI.
R GO; GO:00515; P:protein binding; IPI.
R GO; GO:00515; P:protein binding; IPI.
R R InterPro; IPR003386; Reticulon.
R Ffam; PF02437; Reticulon; 1.
R PROSITE; PS550845; RETICULON; 1.
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NON TER 185
SEQÜENCE 185 AA; 19300 MW; 568DF2FF3EBBF3E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER 1 1 1 SEQUENCE 1245 AA; 135257 MW; 85460D746CE7F16C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kozlowicz A., Doebber A., Trani L.;
"The sequence of Homo sapiens BAC clone RPI1-1255P17.";
submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R.H.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein RTN4 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ä.
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Q7L7Q6 HUMAN
LD Q7L7Q6_HUMAN PRELIMINARY;
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Q53R94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 92.6%
hes 25; Conservative
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NUCLEOTIDE SEQUENCE.
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Best Local Si
Matches 25;
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C93894 HUMAN
D93894 HUMAN
D6 C95894 H
D7  13-58P-20
DE Hypothert
GN Name-RTW
GN 
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NOTECTION SEQUENCES.

REAL TISSUE=Kidney;

REAL TISSUE=Kidney;

REAL STRE=Z388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

REAL STREEZ388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

REAL STREEZ388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

REAL STREEZ388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

REAL STREEZ B. C. Coling F.A. Wagner L., Shemen C.M., Schuler G.D.,

REAL ROWING I., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

REAL ROWING L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

REAL ROWING L., Marusina K.B., Rowing G.,

REAL S.S., Loquellan N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RAPARS S.A., Morkewn P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

RAPARS S.A., Morkewn P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RICHARGS S.W., Maray D.M., Sodercia A.M., Gay L.J., Hulyk S.W.,

RAPARS J., Hellon E., Retteman M., Radain A., Rodrigues S., Sanchez A.,

RAPARS J., Hellon E., Schemen J., Schwichenko Y., Bouffard G.G.,

RAPARS A.C., Grimwood J., Schmutz J., Myers R.M.,

RAPARS A.C., Grimwood J., Schmutz J., Myers R.M.,

RAPARS Schein J.B., Jones S.J.M., Marra M.A.;

RAPARS RAPAR
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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Mammalia; Eutheria; Euarchontoglires;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 80.2%; Score 111.5; DB 2; Length 1 Similarity 85.2%; Pred. No. 0.041; 23; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Van der Putten H.;
Van der Putten H.;
Van der Putten H.;
Exballed (Mry.-2002) to the EMBL/GenBank/DDBJ databases.
ExmBL; AY102275 AAM64246.1; -; meRNA.
EMBL; AY102285 AAM64241.1; -; Genomic_DNA.
GO, GO.0005783; Achdoplasmic reticulum; IEA.
GO, GO.0005783; Achdoplasmic reticulum; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
10-MRY-2005 (TrEMBLrel. 30, Last annotation update)
Reticulon 4, isoform D (RTN4 isoform B2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EPEDEEDEEEDEEDDEDLEELEVL 27
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Cytogenet. Cell Genet. 88:101-102(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                       NUCLECTIDE SEQUENCE.

NUCLECTIDE SEQUENCE.

NUMBELINES-2376540; EUDMed=12488097; DOI=10.1016/S0022-2836 (02)01179-8;
OBTILE 2.7 Huber C., van der Putten H., Schwab M.E.;
NGenomic structure and functional characterisation of the promoters of manan and mouse nogo/rtn4."
NOI. 8101. 328:299-323(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1) TOTALE SEQUENCE (ISOFORMS 1; 2 AND 3).
NUCLECTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;
Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G., Michalovich D., Simmons D.L., Walsh F.S.;
"Inhibitor of neurice outgrowth in humans.";
Nature 403:383-384(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
MEDLINE=21010696; PubMed=11126360; DOI=10.1038/8j.onc.1203948;
MEDLINE=210101696; RinAchita M., Takeda M., Tsujimoto Y.;
Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
Thanovel profesin, RINA-KS, interacts with both Bcl-XL and Bcl-2 on endoplasmic reticulum and reduces their anti-apoptotic activity.";
Oncogene 19:5736-5746 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEB-2005 (Rel. 48, Last amnotation update)
13-SEB-2005 (Rel. 48, Last amnotation update)
(Neutroundor (Neutre outgrowth inhibitor) (Nogo protein) (Foocen)
(Neutroendocrine-specific protein) (NSP) (Neuroendocrine specific protein C homolog) (RTN-x) (Reficulon 5).

Name=RTN4; Synonyma-SSY, KIAA0886, NOGO; ORFNames=My043, SP1507;
Homo sapieng (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RINA HUMAN STANDARD; PRT; 1192 AA.
QSNOC3; O94962; Q9BXGS; Q9H212; Q9H313; Q9UQ42; Q9Y293; Q9Y2Y7;
Q9Y5U6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLECTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
MEDLINE-20237542; PubMed-10773680;
Tang J., Yu L., Bi A.D., Zhao S.-Y.,
"Assignment of the human reticulon 4 gene (RTN4) to chromosome 2p14-->2p13 by radiation hybrid mapping.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 80.2%; Score 111.5; DB 2; Length 392; 1 Similarity 85.2%; Pred. No. 0.043; 23; Conservative 3; Mismatches 0; Indels 1.
                                                                                                                                                                                                                                                                                                                                                              Van der Putten H.;

Dubmitted (NRAT-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BCO16165; AAH16165.1; -; mRNA.

EMBL; AY102278; AAM64247.1; -; mRNA.

EMBL; AY102285; AAM64247.1; -; Genomic_DNA.

GO; GO.065783; C:endoplasmic reticulum; IEA.

InterPro; IPR003388; Reticulon.
                                                                                                           Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dietro; irr.vc.vc.
PROSITE; PSS0845; RETICULON; 1.
PROSITE; PSS0845; RETICULON; 1.
             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Matches
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RAY NUCLECTIDE SEQUENCE [LARGE SCALE WENNA] (ISOFORMS 2 AND 3).

RY TISSUBE-Brain, Eye, Ovary, Pancreas, Placenta, and Skeletal muscle;

RX MEDINES-21886231; PubMed=12477932; DoI=10.103/pnas.242603899;

RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenor L., Marusina K., Farmer A.A., Winbin G.M., Hong L.,

RA Diatchenor L., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Afaba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Hitchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA William M., Madam A.Y. Young A.C., Shevchenorko Y., Bouffard G.G.,

RA Blakesley R.W. Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Schein J.E., Jones E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J. M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J. M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones B.J. M. Marra M.A.,

RA Schnerch A., Schein J.E., Jones B.J. M. Marra M.A.,

RA Schnerch A., Schein J.E., Jones B.J. M. Marra M.A.,

RA Schnerch A., Schein J.E., Jones B.J. M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones W. M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones W. M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones W. M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones W. M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones W. M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones W. M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones W. M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones W. M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones W. M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones W. M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones W. M., Marra M.A.,

RA Schnerch 
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PubMed=15498NCE [LARGE SCALE MENA] (ISOFORM 3).

PubMed=15498NCE [LARGE SCALE MENA] (ISOFORM 3).

Wan D., Gong Y., Qin W., Zhang P., Li J., Wei L., Zhou X., Li H.,

Wan D., Gong Y., Chi W., Zhang P., Li J., Wei L., Zhou X., Li H.,

Gu J.,

Shu H., Chen X., Xu H., Guo M., Pan Z., Chen Y., Ge C., Yang S.,

Gu J.,

"Large-scale cDNA transfection screening for genes related to cancer
development and progression.",
                                                                         Jin W.-L., Ju G.; "Developmentally-regulated alternative splicing in a novel Nogo-A."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Pituitary;
Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
Luo B., Hu R., Chen J.;
"Human neuroendocrine-specific protein C (NSP) homolog gene.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;

MEDLINE-99156230; PubMed=10048485;

MEDLINE-99156230; PubMed=10048485;

Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

Miyajima N., Tanaka A., Kotani H., Suyani N., Nomura N., Ohara O.;

Miyajima N., Tanaka M., Kotani H., Suyani N., Nomura N., Ohara O.;

Miyajima N., Tanaka M., Kotani H., Suyani N., Nomura N., Ohara O.;

Miyajima N., Tanaka M., Kotani H., Suyani N., Nomura N., Ohara O.;

Miyajima N., Tanaka M., Kotani H., Suyani N., Nomura N., Ohara O.;

Miyajima N., Tanaka M., Kotani H., Suyani N., Nomura N., Ohara O.;

Miyajima N., Tanaka M., Kotani H., Suyani N., Nomura N., Ohara O.;

Miyajima N., Tanaka M., Kotani H., Suyani N., Nomura N., Ohara O.;

Miyajima N., Tanaka M., Kotani H., Suyani N., Nomura N., Ohara O.;

Miyajima N., Tanaka M., Kotani H., Suyani N., Nomura N., Nomura N., Ohara O.;

Miyajima N., Tanaka M., Kotani H., Suyani N., Nomura N.
                                                                                                                                                                                                                                                                                                                                                                        NUCLECTIDE SEQUENCE (ISOFORMS 2 AND 3).
TISSUE=Placenta, and Skeletal muscle;
ILO T., Schwartz S.M.;
"Cloning of a member of the reticulon gene family in human.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUCLECTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
TISSUE=lmbilical cord blood;
MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yutsudo M.;
Isolation of a cell death-inducing gene.";
Submitted (UUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [9]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
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sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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NUCLEOTIDE SEQUENCE (ISOFORM 4).
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Search completed: February 17, 2006, 03:55:48
Job time : 125.333 secs
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                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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J. Neurosci. Res. 67:559-565 (2002).

Lock the regeneration of the nervous central system in adults.

Lock the regeneration of the nervous central system in adults.

Lock the regeneration of the new opposition is subcellular.

This is likely consecutive to their change in subcellular.

Location, from the mitrochondria to the endoplasmic reticulum, and sequestration.

Location, from the membrane protein. Endoplasmic reticulum. Anchored to the membrane of the endoplasmic reticulum through 2 putative transmembrane domains.

Location and a sequestration.

Location and sequestrat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name-4; 1800C3-4; Sequence=VSP 005654; Isaally expressed in brain Isofac@QNQC3-4; Seform 1 is specifically expressed in brain TISSUE SPECIFICITY: Isoform 1 is specifically expressed and weakly in heart and skeletal muscler isoform 2 is widely expressed excepted for the liver. Isoform 3 is expressed in brain, skeletal muscle and adipocytes. Isoform 4 is testis-
Shen Y. P. H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G., Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W., Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chon Z., Toloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic Genome Res. 10:1546-1560(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
FOURTHER A. B., GrandPre T., Strittmatter S.M.;
"Identification of a receptor mediating Nogo-66 inhibition of axonal
                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE WENA] OF 482-1192 (ISOFORMS 1/4). TISSUE-Petal brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21888956; PubMed=11891768; DOI=10.1002/jnr.10134;
NG C.E.L., Tang B.L.;
"Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain,

MDDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;

GrandPre=7. Nakamura F., Vartanian T., Strittmatter S.M.;

"Identification of the Nogo inhibitor of axon regeneration as

Reticulon protein.";

Nature 403:439-444(2000).
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CAUTION: Ref.11 sequence differs from that shown due to
frameshifts in positions 1149 and 1156.
                                                                                                                                                                                                                                                                              Mao Y.M., Xie Y., Zheng Z.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                    NUCLECATIDE SEQUENCE OF 186-1192 (ISOFORM 1).
TISSUB-Testis;
Sha J.H., Zhou Z.M., Li J.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:341-346(2001).
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1;
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                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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0
L. 251385; CAB9249.1; -; mRNA.

L. 251385; CAB92250.1; -; mRNA.

EMBL; AB040462; BAB18927.1; -; mRNA.

EMBL; AB040462; BAB18928.1; -; mRNA.

EMBL; AF14857; AAG1176.1; -; mRNA.

EMBL; AF048791, AAG1277.1; -; mRNA.

EMBL; AF087999; AAG1177.1; -; mRNA.

EMBL; AF132049; AAG1177.1; -; mRNA.

EMBL; AF132049; AAG11021.1; -; mRNA.

EMBL; AF132049; AAG11021.1; -; mRNA.

EMBL; AF132049; BAA83112.1; -; mRNA.

EMBL; AF077332; AAG1796.1; -; mRNA.

EMBL; AF077323; AAG1796.1; -; mRNA.

EMBL; BC001035; AAH01035.1; -; mRNA.

TUCY MATCH

80.2*.

est Local Similarity

10.2*.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EPEDEEDEEEEBEEDEEDEELEVL 27
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Sequence 6304, Application US/09513999C

Sequence 6304, Application US/09513999C

Batent No. 6783961

GENERAL INFORMATION:

APPLICANT: Duclert, A.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

FILE REFERENCE: 59.US. REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 6304

LENGTH 68
                          Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 11382, A
Sequence 11383, A
Sequence 4, Appli
Sequence 5, Appli
Sequence 6, Appli
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(9.09-538-092-1018
) Sequence 1018, Application US/09538092
) Sequence 1018, Application US/09538092
) Patent No. 6753314
) GRNEAL INRORMATION:
) APPLICANT: Giot, Loic

APPLICANT: Giot, Loic

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
PILE REPRENCE: 1596-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 1200-03-29
) PRIOR APPLICATION NUMBER: 60/127,352
) PRIOR FILING DATE: 12099-04-01
) RIOR APPLICATION NUMBER: 60/127,352
) RIOR FILING DATE: 1200-02-01
) NUMBER OF SEQ ID NOS: 1387
) SOFTWARE: CURAPATESEGFORMATTER VETSION 0.9
) SEQ ID NO 1018
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80.2%; Score 111.5; DB 2; Length 68;
Best Local Similarity 85.2%; Pred. No. 2.7e-05;
Matches 23; Conservative 3; Mismatches 0; Indels
US-09-949-016-10040
US-08-728-323A-2
US-09-298-568-2
US-09-410-399-2
US-09-410-399-2
US-09-49-016-11382
US-09-949-016-11383
US-08-949-016-11383
US-08-949-016-11383
US-08-949-016-11383
US-08-949-016-11383
US-09-28-70-4
US-09-28-70-4
US-09-214-881A-3
US-09-214-881A-5
US-09-214-881A-5
US-09-214-881A-5
US-09-214-881A-5
US-09-214-881A-5
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US-09-214-881A-5
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           , ORGANISM: Homo sapiens
US-09-513-999C-6304
           g
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9, Appli
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                                                                                                                                                                                      February 17, 2006, 03:56:08; Search time 28.667 Seconds (Without alignments) 77.869 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
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Sequence
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                                         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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1. /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
22. /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3. /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5. /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6. /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-538-092-1018
US-09-244-881A-2
US-09-949-016-10728
US-09-949-016-10728
US-09-949-016-80301
US-09-248-796A-15347
US-09-248-796A-15347
US-09-57-014-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                       US-09-830-972A-2_COPY_31_57
139
1 EPEDEEDBEEEEDBEEDDEDLEELEVL 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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GENERAL INFORMATION:
APPLICANT: Tanil, Rudolph E.
APPLICANT: Tanil, Rudolph E.
APPLICANT: Tanil, Rudolph E.
APPLICANT: Tanil, Rudolph E.
TITLE OF INVENTION: Methods For Modulating Transcription
TITLE OF INVENTION: Methods For Modulating Transcription
TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP)
MUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: 100 New York Ave., NW, Suite 600
CITY: Washington
CONVUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Patentin Release #1.0, Version #1.25
COMPUTER: Patentin Release #1.0, Version #1.25
COMPUTER: Patentin Release #1.0, Version #1.25
CURPUTER: Patentin Release #1.0, Version #1.25
CURPUTER: Patentin Release #1.0, Version #1.25
ATTORNEY ADART: 10000-1994
CLASSIFICATION NUMBER: 36,688
REGISTRATION NUMBER: 36,688
REGISTRATION NUMBER: 0609.4120000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-09-949-016-8301
US-09-949-016-8301
Sequence 8301, Application US/09949016
Sequence 8301, Application US/09949016
Patent No. 681239
Fatent No. 681239
Fatent No. FORMATION:
APPLICANT: VERYER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                             Gaps
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                                                                                                                               Query Match 69.8%; Score 97; DB 2; Length 320;
Best Local Similarity 73.9%; Pred. No. 0.0036;
Matches 17; Conservative 5; Mismatches 1; Indels
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US-08-339-152A-32
i, Sequence 32, Application US/08339152A
Patent No. 5643726
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLLOGY: linear
US-08-339-152A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-371-2540
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10728
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URESULY 4

UR 09-99-016-10728

Sequence 10728, Application US/09949016

Sequence 10728, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION UNMERS: 60/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 10728
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GRAFAL INFORMATION:
GRAFAL INFORMATION:
APPLICANT: Sobajima, Junko
APPLICANT: Goadi, Hickoro
APPLICANT: Tonaka, Masso
APPLICANT: Tranaka, Masso
APPLICANT: Tranaka, Masso
APPLICANT: Sobida, Michiteru
APPLICANT: Sobida, Michiteru
APPLICANT: Sobida, Fundo
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 199-06-07
NUMBER OF SEG ID NOS: 13
SOFTWARE: Patentin Ver: 2.1
SEG ID NOS: 12
LENGTH: 208
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69.8%; Score 97; DB 2; Length 208;
Best Local Similarity 73.9%; Pred. No. 0.0024;
Matches 17; Conservative 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                     Query Match
69.8%; Score 97; DB 2; Length 208;
Best Local Similarity 73.9%; Pred. No. 0.0024;
Matches 17; Conservative 5; Mismatches 1; Indels
                                                                                                          FEATURE:
NAMB/KEY: misc_feature
LOCATION: (0) ... (0)
COTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09214881A Patent No. 6822078 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT; ORGANISM: Homo sapiens
US-09-214-881A-2
                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-09-214-881A-2
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; Requence 9, Application US/09357014
; Patent No. 6291645
; GENERAL INFORMATION:
; APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi
TITLE OF INVENTION: p62 POLYPEPTIDES,
TITLE OF INVENTION: p62 POLYPEPTIDES

AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORREST: 60 State Street, Suite 510
GITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COUNTRY: USA
ZIP: 02109-1875
COUNTRE: LABABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: LBM PC Compatible
COMPUTER: LBM PC LONGY MS-DOS
SOFTWARE: Date: 19-Jul-199
PRIOR APPLICATION NUMBER: 08/574,959
PRIOR APPLICATION NUMBER: 08/574,959
PRIOR APPLICATION NUMBER: 08/574,959
PRIOR STREAM INFORMATION:
NAME: MANGE: MANGE AMP E.
RESERRANCE DOCKET NUMBER: DEN-008
TELEPHONE: (617)-227-7400
COMPUTER REALCH.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.25
SOFTWARE: Petentin ROBE: #1.0, Version #1.25
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: BF.207
REFERINCE/DOCKET NUMBER: BF.009
FELECOMMUNICATION INFORMATION:
TELEPHONE: (517)227-7400
FELESPAN: (517)227-541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.2%; Score 92; DB 1; Best Local Similarity 68.0%; Pred. No. 0.031; Matches 17; Conservative 5; Mismatches
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SEQUENCE CHARACTERISTICS:
LENGTH: 905 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-574-959A-9
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US-09-357-014-9
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Sequence 15347, Application US/09248796A

Sequence 15347, Application US/09248796A

Sequence 15347, Application US/09248796A

General No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT FILING DATE: 1999-02-12

PRIOR PLILING DATE: 1999-02-12

PRIOR PLILING DATE: 1999-02-13

PRIOR PLILING DATE: 1999-02-13

PRIOR PLILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ENTIRE OF SEQ ID NOS: 28208
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Patent No. 596224

Patent No. 1000

APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: Jackyoon Spin, Strominger

ITILE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES

TITLE OF INVENTION: D62 POLYPEPTIDES

TITLE OF INVENTION: D62 POLYPEPTIDES

OORRESPONDRICE ADDRESS:
ADDRESSEE LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2079;
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Best Local Similarity 77.3%; Pred. No. 0.016;
Matches 17; Conservative 4; Mismatches 1; Indels
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66.9%; Score 93; DB 2;
Best Local Similarity 72.0%; Pred. No. 0.053;
Matches 18; Conservative 4; Mismatches
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLILAGION NUMBER: 60/237,768
PRIOR PELICATION NUMBER: 60/237,768
PRIOR PELICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 8301
LENGTH: 2079
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US-09-248-796A-15347
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: USA
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                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8301
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US-08-574-959A-9
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STREET: 60 State Street, Suite 510
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US-09-214-881A-8
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PRT
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US-09-214-881A-8
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                                                                                                                  Gaps
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US-OB-574-959A-7

Sequence 7, Application US/OB574959A

Patent No. 596224

GENERAL INFORMATION:

APPLICANT: Jackyon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: Jackyon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: Jackyon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: Jackyon Shin, Insil Joung, Related POLYPEPTIDES,
ITILE OF INVENTION:

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSES: LAHIVE & COCKFIELD

STREET: Massachusetts

COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/OB/S74,959A

FILING DATE: MANGER: US/OB/S774,959A

APPLICATION NUMBER: 38,207

RESERRECE/DOCKET NUMBER: 38,207

RESERRECE/DOCKET NUMBER: 38,207

RELEPHONE: (617)227-5941

INPORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:

LENGTH: 1135 amino acid

TELEFRANT: Information acid

TOPOLOGY: linear

WOLECULE TYPE: protein
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Patent No. 6291645
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi
and Jack L. Strominger, Strominger TITLE OF INVERTIDES
TITLE OF INVERTIDES
AND USES THEREFOR
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                                                                     Query Match
66.2%; Score 92; DB 2; Length 905;
Best Local Similarity 68.0%; Pred. No. 0.031;
Matches 17; Conservative 5; Mismatches 3; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-357-014-9
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US-09-357-014-7
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US-08-574-959A-7
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APPLICANT: Sobida, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Funicoshi
APPLICANTON: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REPERENCE: OSASS3: Old
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1135;
CITY: Boston
STATE: Wassachusetts
COMPUTRY: USA
COMPUTRY: USA
COMPUTRY: USA
COMPUTRY: USA
COMPUTRY: USA
COMPUTRY: ISA
COMPUTRY: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Intear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-357-014-7
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APPLICANT: Sobajima, Junko
APPLICANT: Useugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masso
APPLICANT: Nakao, Kazuwa
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185 EPEDEEEEEEEDDEDEEEDEDEE 209

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US-09-248-796A-22092

j Sequence 25092, Application US/09248796A

petent No. 6747137

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: WOLCETC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-132

CURRENT FILING DATE: 1999-02-12

PRIOR PAPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR PILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 22092
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Best Local Similarity 73.9%; Pred. No. 0.012;
Matches 17; Conservative 3; Mismatches 3; Indels
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; ORGANISM: Candida albicans
US-09-248-796A-22092
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                                                                                                                                                                    Sequence 10813. Application US/09949016

Sequence 10813. Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT PELING DATE: 2000-14-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-0-09-06

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 10813

LENGTH: 213

WANDER OF SEQ ID NOS: 207012
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APPLICANT: Schoichi
APPLICANT: Schoichi
APPLICANT: Schoichi
APPLICANT: Usesudi, Hiroko
APPLICANT: Tarkahiro
APPLICANT: Tarkahiro
APPLICANT: Tarkahiro
APPLICANT: Tarkahiro
APPLICANT: Tarkahiro
APPLICANT: Schoida Michiteru
APPLICANT: Shirakawa, Hitcshi
APPLICANT: Shirakawa, Hitcshi
APPLICANT: Shirakawa, Hitcshi
APPLICANT: Oshakadi, Pumio
APPLICANT: Oshakadi, Munio
APPLICANT: Oshakadi, Usohi
APPLICANT: Oshida, Michiteru
APPLICANT: Voshida, Michiteru
APPLICANT: Oshida, Michiteru

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; ORGANISM: Sus scrofa
US-09-214-881A-6
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US-09-949-016-10813
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1. /cgn2 6/ptodata/1/pubpaa/NGS0 NEW PUB.pep:*

2. /cgn2 6/ptodata/1/pubpaa/NGS0 NEW PUB.pep:*

3. /cgn2 6/ptodata/1/pubpaa/NGS0 NEW PUB.pep:*

3. /cgn2 6/ptodata/1/pubpaa/NGT NEW PUB.pep:*

5. /cgn2 6/ptodata/1/pubpaa/NGS0 NEW PUB.pep:*

6. /cgn2 6/ptodata/1/pubpaa/NGS0 NEW PUB.pep:*

7. /cgn2 6/ptodata/1/pubpaa/NGS0 NEW PUB.pep:*

7. /cgn2 6/ptodata/1/pubpaa/NGS1 NEW PUB.pep:*

8. /cgn2 6/ptodata/1/pubpaa/NGS1 NEW PUB.pep:*
GenCore version 5.1.7
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                       OM protein
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                                                                                                                                                                                                                                                Title:
Perfect sc
Seguence:
                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ×
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ا د د	2, Appli	30, Appl	1170, Ap	29, Appl	2973, Ap	213, App	1443, Ap	1413, Ap	2651, Ap	1254, Ap	8, Appli	415, App	107, App	1536, Ap	293, App	292, App	4, Appli	3158, Ap	192, App	23, Appl			956, App	954, App	962, App
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Seguence		Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ID	US-11-044-899-2	US-11-044-899-30	US-10-821-234-1170	US-11-044-899-29	US-11-072-512-2973	US-11-169-041-213	US-10-821-234-1443	US-10-821-234-1413	US-11-072-512-2651	US-10-821-234-1254	US-10-528-031-8	US-11-024-959-415	US-11-054-281-107	US-10-821-234-1536	US-11-124-367A-293	US-11-124-367A-292	US-11-166-892-4	US-11-072-512-3158	US-11-169-041-192	US-11-044-111-23	US-10-453-372-964	US-10-453-372-952	US-10-453-372-956	US-10-453-372-954	US-10-453-372-962
80	-	7	9	7	7	7	9	9	7	9	9	7	7	9	7	7	7	7	7	7	9	9	9	9	9
% Query Match Length DB	1163	1163	414	1178	683	773	215	482	687	144	251	345	1229	417	740	760	823	268	879	3375	587	591	591	596	642
& Query Match	100.0	100.0	80.2	80.2	63.3	63.3	62.6	61.9	61.9	60.4	59.7	59.7	59.0	58.3	58.3	58.3	58.3	56.8	56.8	56.1	55.8	55.8	55.8	55.8	55.8
Score	139	139	111.5	111.5	88	88	87	86	86	84	83	83	82	81	81	81	81	79	79	78	77.5	77.5	77.5	77.5	77.5
Result No.		8	m	4	S	v	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

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RESULT 2
US-11-044-899-30
US-11-044-899-30

Sequence 30, Application US/11044899

Publication No. US20050260516A1

Publication No. US20050260516A1

Publication No. US20050260516A1

PUBLICANT: Chen, M.

APPLICANT: Chen, M.

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED

TITLE OF INVENTION: THEREON

PILE REPERENCE: 10200-017-999

CURRENT APPLICATION NUMBER: US/11/044,899

CURRENT PILING DATE: 2005-01-26

PRIOR APPLICATION NUMBER: 09/830,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Sequence 958, App
Sequence 4, Appl
Sequence 950, App
Sequence 970, App
Sequence 970, App
Sequence 122, App
Sequence 122, Appl
Sequence 1409, Ap
Sequence 1169, Ap
Sequence 1167, Ap
Sequence 261, Appl
Sequence 261, App
Sequence 261, App
Sequence 261, App
Sequence 262, App
Sequence 263, App
Sequence 263, App
Sequence 1619, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 139; DB 7;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 27; Conservative 0; Mismatches 0;
  US-10-453-372-958

US-11-156-163-4

US-10-453-372-960

US-10-453-372-960

US-10-453-372-970

US-10-453-372-970

US-10-138-642-4

US-11-128-572-2

US-11-128-572-2

US-11-128-572-2

US-11-128-572-2

US-11-128-100

US-11-124-168A-261

US-11-124-368A-262

US-11-124-368A-262

US-11-124-368A-262

US-11-124-368A-262

US-11-124-368A-262

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US-11-124-368A-263
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    ; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus sp.
US-11-044-899-2
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match 80.2%; Score 111.5; DB 7; Length 1178; Best Local Similarity 85.2%; Pred. No. 2.9e-05; Matches 23; Conservative 3; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.3%; Score 88; DB 7; Length 683; Best Local Similarity 64.0%; Pred. No. 0.0059; Matches 16; Conservative 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OTSUAL TWING.
APPLICANT: MAKAMATSU AI
APPLICANT: WAKAMATSU AI
APPLICANT: WAKAMATSU AI
APPLICANT: SATO, HINOYUKI
APPLICANT: 15HII, SHIZUKO
APPLICANT: 15HII, SHIZUKO
APPLICANT: 15ONO, YUNKO
APPLICANT: 15ONO, YUNKO
APPLICANT: 17OSUKA, KAONU
APPLICANT: 17OSUKA, KAONU
APPLICANT: TOSUKA, KAONU
APPLICANT: TAMEGHIKA, ICHIRO
APPLICANT: TAMEGHIKA, ICHIRO
APPLICANT: TAMEGHIKA, 15HIKO
APPLICANT: TAMEGHIKA, 15HIKO
APPLICANT: TOSUKA, MOTOYUKI
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: WASUHO, YASUHIKO
TITLE OF INVERTION: NOVEL full length CDNA
TITLE OF INVERTION: NOVEL full
APPLICANT: WASUHO, YASUHIKO
TITLE OF INVERTION NUMBER: US (1)/072,512
CURRENT APPLICATION NUMBER: US (0)/350,978
PRIOR PRILING DATE: 2002-01-379298
PRIOR PRILING DATE: 2001-11-05
NUMBER: OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VOYE: 2.1
LENGTH: 683
LENGTH: 683
                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(1178) at all Xaa position
, CTHER INFORMATION: Xaa = any amino acid
US-11-044-899-29
PRIOR FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: 60/107,446
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 51
SOFTWARE FARISEQ for Windows Version 3.0
SEQ ID NO 29
LENGTH: 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EPEDEEDEEEEDEEDEELEVL 27
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Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRGANISM: Homo sapiens
US-11-072-512-2973
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Publication No. US20050260616A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLECTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
TITLE OF INVENTION: THEREON
TITLE OF INVENTION: UNGERE: 2005-01-26
CURRENT APPLICATION NUMBER: US/11/044,899
CURRENT FILING DATE: 2005-01-26
FRICH PAPLICATION NUMBER: 09/830,972
FRICH PRICE ALTON NUMBER: POT/US99/26160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1170, Application US/10821234
; Sequence 1170, Application US/10821234
; Plblication No. US20050255114A1
; GABRAL INFORMATION:
APPLICANT: Stache-Crain, Birgit
APPLICANT: Arache-Crain, Birgit
APPLICANT: Andarmani, Susan
; APPLICANT: NUMBER: US/04/62,047
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SEQ ID NO 1170
; SEQ ID NO 1170
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80.2%; Score 111.5; DB 6; Length 414;
Best Local Similarity 85.2%; Pred. No. 1e-05;
Matches 23; Conservative 3; Mismatches 0; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 139; DB 7; Best Local Similarity 100.0%; Pred. No. 2.9e-08; Matches 27; Conservative 0; Mismatches 0;
      PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION WUMBER: PCT/US99/26160
PRIOR FILING DATE: 1999-11-05
PRIOR PILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 1163
                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)...(1163) at all Xaa position ; OTHER INFORMATION: Xaa = any amino acid US-11-044-899-30
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; ORGANISM: Homo sapiens
US-10-821-234-1170
                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Rattus sp.
                                                                                                                                                                                                                                                                                                                          NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-044-899-29
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Best Local Similarity 56.0%; Pred. No. 0.0097;
Matches 14; Conservative 8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 56.0%; Pred. No. 0.0068;
Matches 14; Conservative 8; Mismatches 3; Indels
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FILE REFERENCE: 821A
CURRENY PAPLICATION NUMBER: US/10/821,234
CURRENY FILING NATE: 2004-04-07
FRIOR APPLICATION NUMBER: US 60/462,047
FRIOR PLING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1413
LENGTH: 482
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Publication No. US20060029945A1
GABREAL INFORMATION:
APPLICANT: SUGITAMA, TOWOYASU
APPLICANT: SUGITAMA, TOWOYASU
APPLICANT: WAKAMATSU, AT
APPLICANT: SATO, HIROYUKI
APPLICANT: SHI, SHIZUKO
APPLICANT: TSHI, SHIZUKO
APPLICANT: TSONO, YUUKO
APPLICANT: HOO, YUK
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147 EEEDDDSEEDEEDDEDEDEDE 171
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US-10-821-234-1254
; Sequence 1254, Application US/10821234
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US-11-072-512-2651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
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                                                                                                                                                                                   APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
TITLE OF INVENTION: CORPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
TITLE OF INVENTION: CELLS
TOTAL OF INVENTION INVENT
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US-10-821-234-1413

US-10-821-234-1413

Sequence 1413, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmani, Susan

APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Best Local Similarity 64.0%; Pred. No. 0.0066;
Matches 16; Conservative 6; Mismatches 3; Indels
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Publication No. US20060019284A1
GENERAL INFORMATION:
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US-10-821-234-1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
US-11-169-041-213
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US-10-821-234-1443
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US-11-054-281-107
US-11-054-281-107
Sequence 107, Application US/11054281
Publication No. US20060013813A1
GENERAL INFORMATION:
ITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-246CIP
CURRENT APPLICATION NUMBER: US/11/054,281
CURRENT APPLICATION NUMBER: 00/261,014
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,013
PRIOR APPLICATION NUMBER: 60/261,026
PRIOR APPLICATION NUMBER: 60/261,026
PRIOR FILING DATE: 2001-01-11
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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
59.7%; Score 83; DB 7; Length 345;
Best Local Similarity 52.2%; Pred. No. 0.01;
Matches 12; Conservative 10; Mismatches 1; Indels
TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS FILE REFERENCE: 044463-0360 CURRENT APPLICATION NUMBER: US/11/024,959 CURRENT FILING DATE: 2004-12-30 PRIOR APPLICATION NUMBER: 60/533,036 PRIOR FILING DATE: 2003-12-30 NUMBER OF SQL ID NOS: 782 SOFTWARE: Patentin version 3.3 SSQ ID NO 415
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US-10-821-234-1536
US-10-821-234-1536
Sequence 1556, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
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, APPLICANT: Stache-Crain, Birgit
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; ORGANISM: Rattus norvegicus
US-11-054-281-107
                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: Pinus radiata
US-11-024-959-415
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Sequence B, Application US/10528031
Sequence B, Application No. US20050262577A1
SEQUENCE WINDORMATION:
Publication No. US20050262577A1
SEQUENCE ORLDIS BIONED Forschungs- und Entwicklungs GmbH
APPLICANT: Guelly, Christian
APPLICANT: Guelly, Christian
APPLICANT: Satloukal, Kurt
APPLICANT: Satloukal, Kurt
APPLICANT: Satloukal, Kurt
APPLICANT: Satloukal, Kurt
APPLICANT: OF INVENTION: Polymptides and nucleic acids encoding these and their use for the TITLE OF INVENTION: Polymptides and nucleic acids encoding these and epithe TITLE OF INVENTION UNMERR: US/10/528,031
CURRENT FILING DATE: 2005-03-16
CURRENT FILING DATE: 2005-03-16
SOSTWARE: PatentIn version 3.1
SEQ ID NOS: 73
SEQ ID NOS: 73
SEQ ID NOS: 73
SEQ ID NOS: 73
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             y Publication No. US20050255114A1
y GENERAL INFORMATION:
APPLICANT: Laber, Ivan
APPLICANT: Laber, Ivan
APPLICANT: Laber, Ivan
APPLICANT: Bache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
TITLE OF INVENTION: Wethods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: WUMBER: US/10/821,234
CURRENT FAPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2003-04-07
RIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE IP SEQ Genes Version 1.0
SEQ ID NO 1254
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US-11-024-959-415
Sequence 415, Application US/11024959
Publication No. US20060010516A1
GENERAL INFORMATION:
APPLICANT: FORSTER, NICHARD L.
APPLICANT: EMERSON, SARAH JANE
APPLICANT: EMERSON, SARAH JANE
APPLICANT: HORGON OLLERN M.
APPLICANT: HUND, STEWN TROY
APPLICANT: MAGUSIN, ANDREAS
APPLICANT: MAGUSIN, ANDREAS
APPLICANT: MAGUSIN, ANDREAS
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CORGANISM: Homo sapiens
US-10-528-031-8
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CORGANISM: Homo sapiens
US-10-821-234-1254
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US-11-14-367A-293

US-11-14-367A-293

US-11-14-367A-293

Sequence 293, Application US/11124367A

Publication No. US20060024700A1

GENERAL INFORMATION

APPLICANT: Michel Cargill

APPLICANT: Hongin Huang

TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof

TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof

TITLE OF INVENTION: Fibrosis Methods of Detection and Uses THEREOF TITLE OF INVENTION: Fibrosis Methods of Detection and Uses THEREOF TITLE OF INVENTION: Fibrosis Wellow of Detection and Uses THEREOF TITLE OF INVENTION NUMBER: US 60/568,846

PRIOR PLING DATE: 2004-05-07

PRIOR PLING DATE: 2004-06-25

PRIOR PLING DATE: 2004-06-25

PRIOR PLING DATE: 2004-06-25

PRIOR PLING DATE: 2004-08-09

NUMBER OF SEQ ID NOS: 34460

SEQ ID NO 293

LENGTH: 740
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT PILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt. SEQ_genes Version 1.0
SEQ ID NO 1536
LENGTH: 417
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58.3%; Score 81; DB 6; Length 417;

Best Local Similarity 56.0%; Pred. No. 0.02;

Matches 14; Conservative 8; Mismatches 3; Indels
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441 BESDEBEBEBEBEBEATDSBEBBLEQMQ 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-11-124-367A-293
                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Homo sapiens
US-10-821-234-1536
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Search completed: February 17, 2006, 04:03:51 Job time : 8.66667 secs

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